

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 08:53:28 ; Search time 7.09576 Seconds

(without alignments)
1545.812 Million cell updates/sec

Title: US-10-791-619-8

Perfect score: 596

Sequence: 1 DIQLTQSPSSLSASVGDRTV.....SHEDPYTFGQGTKEIKRTV 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 498 | 83.6 | 127 | 2 S40367 | Ig kappa chain V-J |
| 2 | 487 | 81.7 | 123 | 2 S40331 | Ig kappa chain - h |
| 3 | 486 | 81.5 | 108 | 2 B49047 | Ig kappa chain V r |
| 4 | 475 | 79.7 | 109 | 2 S31998 | Ig kappa chain - h |
| 5 | 471 | 79.0 | 108 | 2 S44122 | Ig kappa chain V r |
| 6 | 470 | 78.9 | 120 | 2 S46370 | Ig kappa chain V-J |
| 7 | 469 | 78.7 | 108 | 2 S47182 | Ig kappa chain - h |
| 8 | 468 | 78.5 | 109 | 2 S31981 | Ig kappa chain - h |
| 9 | 465.5 | 78.1 | 125 | 2 S40315 | Ig kappa chain - h |
| 10 | 464 | 77.9 | 108 | 1 KIHUHU | Ig kappa chain V-I |
| 11 | 462 | 77.5 | 108 | 2 S19674 | Ig kappa chain V r |
| 12 | 462 | 77.5 | 122 | 2 S40370 | Ig kappa chain - h |
| 13 | 462 | 77.5 | 132 | 2 S40334 | Ig kappa chain - h |
| 14 | 461 | 77.3 | 129 | 2 S52793 | Ig kappa chain V r |
| 15 | 459 | 77.0 | 129 | 2 S52792 | Ig kappa chain V r |
| 16 | 458 | 76.8 | 107 | 2 S36264 | Ig kappa chain V |
| 17 | 457 | 76.7 | 117 | 2 S46371 | Ig kappa chain V-J |
| 18 | 457 | 76.7 | 122 | 2 S40314 | Ig kappa chain - h |
| 19 | 457 | 76.7 | 125 | 2 S40333 | Ig kappa chain V-J |
| 20 | 457 | 76.7 | 129 | 2 S40317 | Ig kappa chain - h |
| 21 | 456.5 | 76.6 | 124 | 2 S40336 | Ig kappa chain V-J |
| 22 | 456 | 76.5 | 129 | 1 KIHUDE | Ig kappa chain V-I |
| 23 | 456 | 76.5 | 109 | 2 S40369 | Ig kappa chain - h |
| 24 | 456 | 76.5 | 131 | 2 S40352 | Ig kappa chain V-J |
| 25 | 455 | 76.3 | 109 | 2 S31979 | Ig kappa chain - h |
| 26 | 455 | 76.3 | 109 | 2 S31978 | Ig kappa chain - h |
| 27 | 454 | 76.2 | 125 | 2 S40350 | Ig kappa chain - h |
| 28 | 453 | 76.0 | 129 | 1 KIHUKV | Ig kappa chain pre |
| 29 | 452 | 75.8 | 126 | 2 S40335 | Ig kappa chain V-J |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 451 | 75.7 | 109 | 2 S31980 | Ig kappa chain - h |
| 31 | 451 | 75.7 | 125 | 2 S40349 | Ig kappa chain V-J |
| 32 | 450 | 75.5 | 108 | 1 KIHUOU | Ig kappa chain V-I |
| 33 | 450 | 75.5 | 130 | 2 S40368 | Ig kappa chain - h |
| 34 | 449.5 | 75.4 | 107 | 2 S36275 | Ig lambda chain V |
| 35 | 449 | 75.3 | 107 | 2 JLO139 | Ig kappa chain V r |
| 36 | 448 | 75.2 | 109 | 2 S32001 | Ig kappa chain - h |
| 37 | 448 | 75.2 | 109 | 2 S31983 | Ig kappa chain - h |
| 38 | 448 | 75.2 | 128 | 2 S46372 | Ig light chain var |
| 39 | 447 | 75.0 | 108 | 2 S31977 | Ig kappa chain - h |
| 40 | 447 | 75.0 | 117 | 2 S46376 | Ig kappa chain V-J |
| 41 | 447 | 75.0 | 125 | 2 S40316 | Ig kappa chain - h |
| 42 | 445 | 74.7 | 108 | 1 KIHUAV | Ig kappa chain V-I |
| 43 | 445 | 74.7 | 108 | 1 KIHURN | Ig kappa chain V-I |
| 44 | 443 | 74.3 | 108 | 1 KIHULY | Ig kappa chain V-I |
| 45 | 443 | 74.3 | 129 | 2 S52789 | Ig kappa chain V r |

ALIGNMENTS

RESULT 1

S40367

Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40367

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40367

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-127 <KLE>

A:Cross-references: EMBL:X72477

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 498; DB 2; Length 127;
Best Local Similarity 85.1%; Pred. No. 1.3e-36;
Matches 97; Conservative 5; Mismatches 5; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASKVDGDSYLNWYQOKPKAKPLLIYAASYLES 60
DB 18 DIQMTQSPSSLSASVGDRTVITCRASQSI----SNLWYQOKPKAKPLLIYAASSLQS 73
QY 61 GVPGRFSGSGSGTDTLTITSLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114
DB 74 GVPGRFSGSGSGTDTLTITSLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 127

RESULT 2

S40331

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40331

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40331

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-123 <KLE>

A:Cross-references: EMBL:X72441; NID:G441350; PIDN:CAA51109.1; PID:G441351

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 487; DB 2; Length 123;

```
Best Local Similarity 86.5%; Pred. No. 1.2e-35;
Matches 96; Conservative 5; Mismatches 6; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGRVVTITCRASPKVDGEGSYLNWYQKPGKAPKLLIYAASLYLES 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 17 DIQWTQSPSSLSASVGRVVTITCRASQSI-----SSYLNWYQKPGKAPKLLIYAASLSQS 72
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

QY 61 GVPSRFSGSGGTDTFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIK 111
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 73 GVPSRFSGSGGTDTFTLTISLQPEDFATYYCQSYSTPRTFGGTKVEIK 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 3
B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B49047
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A;Reference number: A49047; MUID:92387224; PMID:1516616
A;Accession: B49047
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-108 <VIC>
A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
A;Experimental source: thymic B lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIPI:113209)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 486; DB 2; Length 108;
Best Local Similarity 85.7%; Pred. No. 1.2e-35;
Matches 96; Conservative 5; Mismatches 7; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGRVVTITCRASPKVDGEGSYLNWYQKPGKAPKLLIYAASLYLES 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 1 DIQWTQSPSSLSASVGRVVTITCRASQSI-----SSYLNWYQKPGKAPKLLIYAASLSQS 56
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

QY 61 GVPSRFSGSGGTDTFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIKR 112
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 57 GVPSRFSGSGGTDTFTLTISLQPEDFATYYCQSYSTPLTFGGTKVEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 4
S31998
Ig kappa chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S31998
R;Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A;Reference number: S31977
A;Accession: S31998
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-109 <POR>
A;Cross-references: EMBL:Z15081; NID:g38501; PIDN:CAA78790.1; PID:g38502
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 475; DB 2; Length 109;
Best Local Similarity 80.5%; Pred. No. 1.1e-34;
Matches 91; Conservative 12; Mismatches 6; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGRVVTITCRASPKVDGEGSYLNWYQKPGKAPKLLIYAASLYLES 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 1 ELVWTQSPSSLSASVGRVVTITCRASQSI-----SAYLNWYQKPGKAPKLLIYAASLSQS 56
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

QY 61 GVPSRFSGSGGTDTFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIKRT 113
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
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Db 57 GVPSRFSGSGGTDTFTLTISLQPEDFATYYCQSYDTPWTFGHGTVKEIKRT 109
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 5
S44122
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44122
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable re
A;Reference number: S44105
A;Accession: S44122
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <HAW>
A;Cross-references: EMBL:Z31390; NID:g472976; PIDN:CAA83265.1; PID:g940533
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 471; DB 2; Length 108;
Best Local Similarity 83.0%; Pred. No. 2.5e-34;
Matches 93; Conservative 7; Mismatches 8; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGRVVTITCRASPKVDGEGSYLNWYQKPGKAPKLLIYAASLYLES 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 1 DIQWTQSPSSLSASVGRVVTITCRASQSI-----SSYLNWYQKPGKAPKLLIYAASLSQS 56
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

QY 61 GVPSRFSGSGGTDTFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIKR 112
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 57 GVPSRFSGSGGTDTFTLTISLQPEDFATYYCQSYSTPWTTFGGTKVEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 6
S46370
Ig kappa chain V-J region (T23-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S46370; S38644
R;Bensimon, C.; Chaatagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
A;Reference number: S46369; MUID:94313975; PMID:8039491
A;Accession: S46370
A;Molecule type: mRNA
A;Residues: 1-120 <BEN>
A;Cross-references: EMBL:Z27171; NID:g415957; PIDN:CAA81695.1; PID:g415958
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;26-100/Domain: immunoglobulin homology <IMM>

Query Match 78.9%; Score 470; DB 2; Length 120;
Best Local Similarity 81.6%; Pred. No. 3.4e-34;
Matches 93; Conservative 8; Mismatches 7; Indels 6; Gaps 2;

QY 1 DIQLTQSPSSLSASVGRVVTITCRASPKVDGEGSYLNWYQKPGKAPKLLIYAASLYLES 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 11 DIQWTQSPSSLSASVGRVVTITCRASRSI-----SSFLNWYQKPGKAPQLLIYASRLQS 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

QY 61 GVPSRFSGSGGTDTFTLTISLQPEDFATYYCQOSHEDP--YTFGQGTKEIKR 112
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 67 GVPSRFSGSGGTDTFTLTISLQPEDFATYYCQSFNPPEYTFGGTKLEINR 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 7
S47182
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47182
```


A:Molecule type: mRNA
A;Residues: 1-108 <MAR>
A;Cross-references: EMBL:X61642; NID:g937860; PIDN:CAA43823.1; PID:g1335386
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 462; DB 2; Length 108;
Best Local Similarity 81.2%; Pred. No. 1.5e-33;
Matches 91; Conservative 9; Mismatches 8; Indels 4; Gaps 1;

QY 1 DIQLTQPSSLSASVGRVTITCRASKPVDGDSYLNNWYOOKPGKAPKLIIYAASYLES 60
 :|::||| | ||||| ::| :|::||| | ||||| ::| :|::||| | ||||| ::| :|:
DB 1 EIULTQPSSLSASVGRVTITCRASSQSI---SNLYNWYOOKPGKAPKLIIYAASTLQS 56

QY 61 GVPSRFGSGSGTDFTLTISGLPEDPATYYCCOSHEDPYTFGGGTKEIKR 112
 :|::||| | ||||| ::| :|::||| | ||||| ::| :|::||| | ||||| ::| :|:
DB 57 GVPSRFGSGSGTDFTLTINSLPEDPATYYCCQTNSFPFLTFFGGGTKEIKR 108

RESULT 12
S40370
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40370
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40370
A;Status: preliminary; translation not shown
A:Molecule type: mRNA
A;Residues: 1-122 <KLE>
A;Cross-references: EMBL:X72480; NID:g441428; PIDN:CA51148.1; PID:g441429
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-104/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 462; DB 2; Length 122;
Best Local Similarity 82.1%; Pred. No. 1.7e-33;
Matches 92; Conservative 7; Mismatches 9; Indels 4; Gaps 1;

QY 1 DIQLTQPSSLSASVGRVTITCRASKPVDGDSYLNNWYOOKPGKAPKLIIYAASYLES 60
 :|::||| | ||||| ::| :|::||| | ||||| ::| :|::||| | ||||| ::| :|:
DB 15 DIQLTQPSSLSASVGRVTITCRASSQI----STFLHWYQQNLGXKAPKLIIYAASNLOS 70

QY 61 GVPSRFGSGSGTDFTLTISGLPEDPATYYCCOSHEDPYTFGGGTKEIKR 112
 :|::||| | ||||| ::| :|::||| | ||||| ::| :|::||| | ||||| ::| :|:
DB 71 GVPSRFGSGSGTDFTLTISGLPEDPATYYCCOSYTTPRTFFGGGTKEIKR 122

RESULT 13
S40334
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40334
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40334
A;Status: preliminary; translation not shown
A:Molecule type: mRNA
A;Residues: 1-132 <KLE>
A;Cross-references: EMBL:X72444
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 462; DB 2; Length 132;
Best Local Similarity 79.8%; Pred. No. 1.9e-33;
Matches 91; Conservative 9; Mismatches 8; Indels 4; Gaps 1;

Search completed: June 3, 2005, 09:17:50
Job time : 8.09576 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2005, 08:31:37 ; Search time 32.7497 Seconds
(without alignments)
1782.523 Million cell updates/sec

Title: US-10-791-619-8
Perfect score: 596
Sequence: 1 DIQLTQSPSSLSASVGRVT.....SHEDPYTFGQTKVIEKRTV 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % | Length | DB | ID | Description |
|------------|-------|---------|--------|----|------------|---------------------|
| 1 | 481 | 80.7 | 236 | 2 | Q6GMX8 | Q6gmX8 homo sapien |
| 2 | 480 | 80.5 | 108 | 2 | Q9UL77 | Q9ul77 homo sapien |
| 3 | 470 | 78.9 | 236 | 2 | Q6GMW1 | Q6gmW1 homo sapien |
| 4 | 468.5 | 78.6 | 107 | 2 | Q96SA9 | Q96sa9 homo sapien |
| 5 | 466 | 78.2 | 236 | 2 | Q6GMX0 | Q6gmX0 homo sapien |
| 6 | 465 | 78.0 | 236 | 2 | Q6PIH7 | Q6pih7 homo sapien |
| 7 | 464 | 77.9 | 108 | 1 | KV1H_HUMAN | P01600 homo sapien |
| 8 | 456 | 76.5 | 108 | 1 | KV1E_HUMAN | P01597 homo sapien |
| 9 | 453 | 76.0 | 129 | 1 | KV1W_HUMAN | P04431 homo sapien |
| 10 | 450 | 75.5 | 108 | 1 | KV1N_HUMAN | P01606 homo sapien |
| 11 | 446 | 74.8 | 236 | 2 | Q723Y4 | Q723y4 homo sapien |
| 12 | 445 | 74.7 | 108 | 1 | KV1B_HUMAN | P01594 homo sapien |
| 13 | 445 | 74.7 | 108 | 1 | KV1V_HUMAN | P04430 homo sapien |
| 14 | 443.5 | 74.4 | 107 | 2 | Q9UL81 | Q9ul81 homo sapien |
| 15 | 443 | 74.3 | 108 | 1 | KV1M_HUMAN | P01605 homo sapien |
| 16 | 442 | 74.2 | 108 | 2 | Q9UL70 | Q9ul70 homo sapien |
| 17 | 442 | 74.2 | 234 | 2 | Q72473 | Q72473 homo sapien |
| 18 | 441 | 74.0 | 111 | 1 | KV3M_MOUSE | P01665 mus musculus |
| 19 | 440 | 73.8 | 108 | 1 | KV1K_HUMAN | P01603 homo sapien |
| 20 | 440 | 73.8 | 108 | 1 | KV1O_HUMAN | P01607 homo sapien |
| 21 | 438 | 73.5 | 108 | 1 | KV1S_HUMAN | P01611 homo sapien |
| 22 | 437 | 73.3 | 236 | 2 | Q6GMX9 | Q6gmX9 homo sapien |
| 23 | 436 | 73.2 | 108 | 1 | KV1P_HUMAN | P01598 homo sapien |
| 24 | 436 | 73.2 | 108 | 1 | KV1G_HUMAN | P01599 homo sapien |
| 25 | 436 | 73.2 | 108 | 1 | KV1Y_HUMAN | P01662 homo sapien |
| 26 | 436 | 73.2 | 111 | 1 | KV3O_MOUSE | P01667 mus musculus |
| 27 | 434 | 72.8 | 108 | 1 | KV1P_HUMAN | P01608 homo sapien |
| 28 | 434 | 72.8 | 111 | 1 | KV3N_MOUSE | P01666 mus musculus |
| 29 | 434 | 72.8 | 236 | 2 | Q6PII5 | Q6pii5 homo sapien |
| 30 | 433 | 72.7 | 108 | 1 | KV1R_HUMAN | P01610 homo sapien |
| 31 | 433 | 72.7 | 111 | 1 | KV3L_MOUSE | P01664 mus musculus |

| | | | | | | |
|----|-------|------|-----|---|------------|---------------------|
| 32 | 433 | 72.7 | 111 | 1 | KV3Q_MOUSE | P01669 mus musculus |
| 33 | 431 | 72.3 | 108 | 2 | Q9UL79 | Q9ul79 homo sapien |
| 34 | 429 | 72.0 | 108 | 1 | KV1L_HUMAN | P01604 homo sapien |
| 35 | 429 | 72.0 | 236 | 2 | Q6PIH4 | Q6pih4 homo sapien |
| 36 | 427 | 71.6 | 116 | 2 | Q96PF6 | Q96pf6 homo sapien |
| 37 | 427 | 71.6 | 244 | 2 | Q65ZC8 | Q65zc8 homo sapien |
| 38 | 425 | 71.3 | 108 | 1 | KV1A_HUMAN | P01593 homo sapien |
| 39 | 424.5 | 71.2 | 107 | 1 | KV1D_HUMAN | P01596 homo sapien |
| 40 | 423.5 | 71.1 | 109 | 1 | KV1T_HUMAN | P01612 homo sapien |
| 41 | 423 | 71.0 | 111 | 1 | KV3H_MOUSE | P01660 mus musculus |
| 42 | 423 | 71.0 | 240 | 2 | Q65ZC9 | Q65zc9 homo sapien |
| 43 | 422 | 70.8 | 108 | 1 | KV1Q_HUMAN | P01609 homo sapien |
| 44 | 422 | 70.8 | 111 | 2 | Q81IU6 | Q81iu6 mus musculus |
| 45 | 421 | 70.6 | 108 | 1 | KV1C_HUMAN | P01595 homo sapien |

ALIGNMENTS

RESULT 1

| ID | Q6GMX8 | PRELIMINARY; | PRT; | 236 AA. |
|----|--------------------------------------------------------------------------------|--------------|------|---------|
| AC | Q6GMX8; | | | |
| DT | 05-JUL-2004 (Tremblrel. 27, Created) | | | |
| DT | 05-JUL-2004 (Tremblrel. 27, Last sequence update) | | | |
| DT | 05-JUL-2004 (Tremblrel. 27, Last annotation update) | | | |
| DE | Hypothetical protein. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Primary B-Cells; | | | |
| RX | MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899; | | | |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., | | | |
| RA | Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., | | | |
| RA | Altechul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F., | | | |
| RA | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., | | | |
| RA | Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., | | | |
| RA | Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., | | | |
| RA | Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., | | | |
| RA | Raha S.S., Locquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., | | | |
| RA | Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., | | | |
| RA | Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., | | | |
| RA | Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A., | | | |
| RA | Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., | | | |
| RA | Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., | | | |
| RA | Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., | | | |
| RA | Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., | | | |
| RA | Krzywinski M.I., Skalska U., Smalusi D.E., Schnerch A., Schein J.E., | | | |
| RT | Jones S.J., Marra M.A.; | | | |
| RT | "Generation and initial analysis of more than 15,000 full-length human | | | |
| RT | and mouse cDNA sequences." | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). | | | |
| RL | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Primary B-Cells; | | | |
| RA | Strausberg R.; | | | |
| RL | Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases. | | | |
| DR | EMBL; BC073764; AAH73764.1; - | | | |
| DR | InterPro; IPR003599; IG. | | | |
| DR | InterPro; IPR007110; IG-like. | | | |
| DR | InterPro; IPR003597; IG c1. | | | |
| DR | InterPro; IPR003006; IG_MHC. | | | |
| DR | InterPro; IPR003596; IG_v. | | | |
| DR | Pfam; PF07654; Cl-set; 1. | | | |
| DR | Pfam; PF00047; IG; 2. | | | |
| DR | SMART; SM00409; IG; 2. | | | |
| DR | SMART; SM00407; IGc1; 1. | | | |
| DR | SMART; SM00406; IGv; 1. | | | |
| DR | PROSITE; PS50835; IG_LIKE; 2. | | | |
| DR | PROSITE; PS00290; IG_MHC; UNKNOWN_1. | | | |

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KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match      80.7%; Score 481; DB 2; Length 236;
Best Local Similarity 82.5%; Pred. No. 6.3e-40;
Matches 94; Conservative 9; Mismatches 7; Indels 4; Gaps 1;

Qy 1 DIQQTQSPSSLSASVGRVITTCRASKPVDCGDSYLNWYQKPGKAPKLLIYAASYLE 60
Db 23 DIQMTQSPSSVSASVGRVITTCRASQGI---SSSLAWYQKPGKAPKLLIYAASLSQ 78

Qy 61 GVPFRFSGSGGTDFTLTITSLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114
Db 79 GVPFRFSGSGGTDFTLTITSLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 132

RESULT 2
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RL MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSP; P01607; 1BWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match      80.5%; Score 480; DB 2; Length 108;
Best Local Similarity 83.9%; Pred. No. 3.3e-40;
Matches 94; Conservative 7; Mismatches 7; Indels 4; Gaps 1;

Qy 1 DIQQTQSPSSLSASVGRVITTCRASKPVDCGDSYLNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQMTQSPSSLSASVGRVITTCRASQGI---SSSLWYQKPGKAPKLLIYAASLSQ 56

Qy 61 GVPFRFSGSGGTDFTLTITSLQPEDPATYCCQSHEDPYTFGQGTKEIKR 112
Db 57 GVPFRFSGSGGTDFTLTITSLQPEDPATYCCQSHEDPYTFGQGTKEIKR 108

RESULT 3
Q6GMW1 PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Query Match      78.9%; Score 470; DB 2; Length 236;
Best Local Similarity 82.3%; Pred. No. 7.9e-39;
Matches 93; Conservative 7; Mismatches 9; Indels 4; Gaps 1;

Qy 2 IQLTQSPSSLSASVGRVITTCRASKPVDCGDSYLNWYQKPGKAPKLLIYAASYLESG 61
Db 24 IQMTQSPSSLSASVGRVITTCRASQGI---LCWYQKPGKAPKLLIYAASLSQSG 79

Qy 62 VPSRFSGSGGTDFTLTITSLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114
Db 80 VPSRFSGSGGTDFTLTITSLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 132

RESULT 4
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```


| | |
|-----------------------|------------------------------------------------------------------------|
| RP | SEQUENCE FROM N.A. |
| RC | TISSUE=Spleen; |
| RA | Strausberg R.; |
| RL | Submitted (JUN-2004) to the EMBL/GenBank/DBDJ databases. |
| DR | EMBL; BC073775; AAH73775.1; - |
| DR | InterPro; IPR003599; Ig |
| DR | InterPro; IPR007110; Ig-like |
| DR | InterPro; IPR003597; Ig-cl |
| DR | InterPro; IPR003006; Ig_MHC |
| DR | InterPro; IPR003596; Ig_V |
| DR | Pfam; PF00654; Cl-set; 1 |
| DR | Pfam; PF00047; ig; 2 |
| DR | SMART; SM00409; IG; 2 |
| DR | SMART; SM00407; IGcl; 1 |
| DR | SMART; SM00406; IGV; 1 |
| DR | PROSITE; PSS0835; IG_LIKE; 2 |
| DR | PROSITE; PS00290; IG_MHC; UNKNOWN_1 |
| KW | Hypothetical protein_KW |
| SQL | Sequence 236 AA; 25907 MW; 864EA08C7E92BF9F CRC64; |
| | |
| Query Sequence | 78.2%; Score 466; DB 2; Length 236; |
| Best Local Similarity | 80.7%; Pred. No. 2e-38; |
| Matches | 92; Conservative 9; Mismatches 9; Indels 4; Gaps 1 |
| | |
| Qy | 1 DIQLTQPSSLSASVGRVRVTTCASFPDVGDSYLNWVOOKGKAPKLIIYAASYLES 60 |
| Dd | 23 DIQWTQPSLSASVGRVRVTITCRASQNI-----NNYLNWYQLKFGKAPNLIIYAASSLQS 78 |
| | |
| Qy | 61 GVPSRPSGSGSGDTFTLTISLPDPEDPATYYCQOSHEDPVTFFGGTKVEIKRTV 114 |
| Dd | 79 GVPSRPSGSGSGDTFTLTISLSLRDDPATYYCQSYNIPITFGGTNVIEIKRTV 132 |
| | |
| RESULT 6 | |
| Q6PIH7 | ID Q6PIH7 PRELIMINARY; PRT; 236 AA. |
| AC | Q6PIH7 |
| DT | 05-JUL-2004 (TrEMBLrel. 27, Created) |
| DT | 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) |
| DE | 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) |
| DE | Hypothetical protein. |
| OS | Homo sapiens (Human). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |
| OX | NCBI_TaxID=9606; |
| RN | [1] |
| RN | SEQUENCE FROM N.A. |
| RC | TISSUE=Lung; |
| RX | MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899; |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., |
| RA | Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., |
| RA | Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., |
| RA | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F., |
| RA | Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L., |
| RA | Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., |
| RA | Brownstein M.J., Uedin T.B., Toshilyuki S., Carninci P., Prange C., |
| RA | Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., |
| RA | Besak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., |
| RA | Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., |
| RA | Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., |
| RA | Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., |
| RA | Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., |
| RA | Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., |
| RA | Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., |
| RA | Krzywinski M.I., Stalska U., Smailus D.E., Schnerch A., Schein J.E., |
| RA | Jones S.J., Marra M.A.; |
| RT | "Generation and initial analysis of more than 15,000 full-length human |
| RT | and mouse cDNA sequences."; |
| FL | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). |
| RN | [2] |
| RN | SEQUENCE FROM N.A. |
| RP | TISSUE=Lung; |
| RA | Strausberg R.; |

| | |
|---------------|------------------------|
| KV1W_HUMAN | |
| ID_KV1W_HUMAN | STANDARD; PRT; 129 AA. |
| AC_P04431; | |

13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG kappa chain V-I region Walker precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; KIHUWK.
DR HSSP; P01607; 1BWW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 Ig kappa chain V-I region Walker.
FT DOMAIN 23 45 Framework-1.
FT DOMAIN 46 56 Complementarity-determining-1.
FT DOMAIN 57 71 Framework-2.
FT DOMAIN 72 78 Complementarity-determining-2.
FT DOMAIN 79 110 Framework-3.
FT DOMAIN 111 119 Complementarity-determining-3.
FT DOMAIN 120 129 Framework-4.
FT DISULFID 45 110 By similarity.
FT NON TER 129 129
SQ SEQUENCE 129 AA; F941FA07D4AFC2F9 CRC64;

Query Match 76.0%; Score 453; DB 1; Length 129;
Best Local Similarity 81.1%; Pred. No. 2e-37;
Matches 90; Conservative 8; Mismatches 9; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGRVTITCRASKPVDGSGSYLNWYQKPKAPKLIYAASYLE 60
Db 23 DIQMTQSPSSLSASVGRVTITCRASQSI-----SNLYNWYQKPKAPKLIYAASLSQ 78
Qy 61 GVPFRFSGSGSGTDFTLTISLQPEDFATYTCQSHEDPYTFGQGTKEIK 111
Db 79 GVTFRFSGSGSGTDFTLTISLQPEDSATYTCQSYSTLTITFGQGTLEIK 129

RESULT 10
KV1N HUMAN
ID KVIN HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-I region OU.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
chains.";
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenström's
macroglobulin.
DR PIR; A01872; KIHUOU.
DR HSSP; P01607; 1BWW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 8283D4A24105827E CRC64;

Query Match 75.5%; Score 450; DB 1; Length 108;
Best Local Similarity 71.4%; Pred. No. 3.3e-37;
Matches 80; Conservative 19; Mismatches 9; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGRVTITCRASKPVDGSGSYLNWYQKPKAPKLIYAASYLE 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASZTI-----SYLBNWYQKPKAPKLIYAASBLHS 56
Qy 61 GVPFRFSGSGSGTDFTLTISLQPEDFATYTCQSHEDPYTFGQGTKEIKR 112
Db 57 GVPFRFSGSGSGTBTFTTISLZPZBFATYTCZZSYSPFTFGZTRLZIKR 108

RESULT 11
Q7Z3Y4
ID Q7Z3Y4 PRELIMINARY; PRT; 236 AA.
AC Q7Z3Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussidi T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.O., Lu X., Gibbs R.A.,

| | |
|---------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| | PIR; A9L653; KIHUAU. |
| DR | PDB; IJVS; X-ray; A=1-107. |
| DR | GO; GO:0005576; C:extracellular; NAS. |
| DR | GO; GO:0003823; F:antigen binding; NAS. |
| DR | GO; GO:0006955; P:immune response; NAS. |
| DR | InterPro; IPRO07110; Ig-like. |
| DR | InterPro; IPO003596; Ig_v. |
| DR | Ffam; PF00047; IG; 1. |
| DR | SMART; SM00406; IGV; 1. |
| DR | PROSITE; PS08315; IG LIKE; 1. |
| KW | 3D-structure; Bence-Jones protein, Direct protein sequencing; |
| KW | Immunoglobulin V region. |
| KX | DOMAIN 1 23 Framework-1. |
| FT | DOMAIN 24 34 Complementarity-determining-1. |
| FT | DOMAIN 35 49 Framework-2. |
| FT | DOMAIN 50 56 Complementarity-determining-2. |
| FT | DOMAIN 57 88 Framework-3. |
| FT | DOMAIN 89 97 Complementarity-determining-3. |
| FT | DOMAIN 98 107 Framework-4. |
| FT | DISULFID 23 88 By similarity. |
| FT | STRAND 4 5 |
| FT | STRAND 10 13 |
| FT | TURN 15 16 |
| FT | TURN 19 25 |
| FT | TTURN 30 31 |
| FT | STRAND 33 38 |
| FT | TTURN 40 41 |
| FT | STRAND 44 49 |
| FT | TTURN 50 52 |
| FT | STRAND 53 54 |
| FT | TTURN 56 57 |
| FT | TTURN 60 61 |
| FT | STRAND 62 67 |
| FT | TTURN 68 69 |
| FT | STRAND 70 75 |
| FT | HELIX 80 82 |
| FT | STRAND 85 90 |
| FT | STRAND 97 98 |
| FT | STRAND 102 106 |
| FT | NON_TER 108 108 |
| SQ | SEQUENCE 108 AA; ILI939 MW; E80LLI187EE6PFB9 CRC64; |
| | Query Match 74.7%; Score 445; DB 1; Length 108; |
| | Best Local Similarity 79.5%; Pred. No. le-36; |
| Matches | 89; Conservative 5; Mismatches 14; Indels 4; Gaps 3 |
| Qy | 1 DIQLQTSPSSLSASVGRVTITTCRASKEVDGEGSYLNWYQQKPKAPKLIIYAASYLES 60 : 1 DIQMTPSPPSLASVSGDVRTITCQASDI---SDLYNMYQQKPGKAPKLIIYASNLES 56 |
| Db | 61 GVPSRFSGSGCTDTLTITSILOPEDRATYYCQSHEDPYTFGGTKVEIKR 112 |
| Db | 57 GVPSRFGSGGSNAHFTTITSILOPEAIATYYCCQDYLPWFTEGGTGKVEIKR 108 |
| RESULT | 13 |
| XIV_HUMAN | |
| ID_KIV_HUMAN STANDARD; PR; 108 AA. | |
| AC PO4430; | |
| DT 13-AUG-1987 (Rel. 05, Created) | |
| DT 13-AUG-1987 (Rel. 05, Last sequence update) | |
| DT 05-JUL-2004 (Rel. 44, Last annotation update) | |
| DE Ig kappa chain V-I region BAN. | |
| OS Homo sapiens (Human). | |
| OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | |
| OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | |
| OX NCBI_TaxID=9606; | |
| RN [1] | |
| RP SEQUENCE. | |
| RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2; | |
| RA Dulet F.E., O'Connor T.P., Benson M.D.; | |
| RL "Polymorphism in a kappa I primary (AL) amyloid protein (BAN)."; Mol. Immunol. 23:73-78(1986). | |

DR PIR: A01878; K1HUBN.
DR HSSP: P80362; 1WTL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Amyloid; Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 74.7%; Score 445; DB 1; Length 108;
Best Local Similarity 79.5%; Pred. No. 1e-36;
Matches 89; Conservative 8; Mismatches 11; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGDRTVITTCRASKPVVDGEGSYLNWYQOKPGKAPKLLIYAASYLES 60
Db 1 DIQLTQSPSSLSASVGDRTVITTCRASQSV----YNYVAMFOQKPGKAPKSLIYDASTLQS 56

Qy 61 GVPSRFSGSGSGTDTLTITSLQPEDFATYYCQSHEDPYTFGQTKVEIKR 112
Db 57 GVPNFTGSGSGTDTLTITSLQPEDFATYYCQYNSPYTFGQTKVQIKR 108

RESULT 14

Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DR 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RA Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.;
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035033; AAD56269.1; --
DR HSSP: P01607; 1BW.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IGV_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 74.4%; Score 443.5; DB 2; Length 107;
Best Local Similarity 79.5%; Pred. No. 1.5e-36;
Matches 89; Conservative 8; Mismatches 10; Indels 5; Gaps 2;

Qy 1 DIQLTQSPSSLSASVGDRTVITTCRASKPVVDGEGSYLNWYQOKPGKAPKLLIYAASYLES 60
Db 1 DIQLTQSPSSLSASVGDRTVITTCRASQSI-----SNYLNWYQOKPGKAPNLLIYAASLQS 56

Qy 61 GVPSRFSGSGSGTDTLTITSLQPEDFATYYCQSHEDPYTFGQTKVEIKR 112
Db 57 GVPNFTGSGSGTDTLTITSLQPEDFATYYCQYNSPYTFGQTKVQIKR 107

RESULT 15

KVLM_HUMAN
ID KVLM_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human IgM anti-gamma globulins (Lay/Pom) with shared idiotypic specificities."; Scand. J. Immunol. 5:677-684(1976).
RL CC -! MISCELLANEOUS: The second and third hypervariable regions of this chain are identical with those of the human POM V-III kappa chain, with which it shares certain idiotypic determinants.
CC -! MISCELLANEOUS: This chain was isolated from an IGM with anti-gamma globulin activity.
CC PIR: A01871; K1HULY.
DR HSSP: P01607; 1BW.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IGV_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 74.3%; Score 443; DB 1; Length 108;
Best Local Similarity 78.6%; Pred. No. 1.6e-36;
Matches 88; Conservative 8; Mismatches 12; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGDRTVITTCRASKPVVDGEGSYLNWYQOKPGKAPKLLIYAASYLES 60
Db 1 DIQLTQSPSSLSASVGDRTVITTCRASQSV----NAYLNWYQOKPGKAPKLLIYGASTREA 56

Qy 61 GVPSRFSGSGSGTDTLTITSLQPEDFATYYCQSHEDPYTFGQTKVEIKR 112
Db 57 GVPNFTGSGSGTDTLTITSLQPEDATYYCQYNNWPPPTFGQTKVEIKR 108

Search completed: June 3, 2005, 09:16:13
Job time : 33.7497 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 08:29:47 ; Search time 37.3502 Seconds
(without alignments)
1180.467 Million cell updates/sec

Title: US-10-791-619-8
Perfect score: 596
Sequence: 1 DIQLTQSPSSLSASVGRDVT.....SHEDPYTFGQTKVEIKRTV 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 596 | 100.0 | 114 | 4 | AAB76942 Variable |
| 2 | 596 | 100.0 | 114 | 8 | ADN07029 Anti-IGE |
| 3 | 596 | 100.0 | 218 | 2 | AAW95664 Mus muscu |
| 4 | 596 | 100.0 | 218 | 2 | AAW95669 Mus muscu |
| 5 | 596 | 100.0 | 218 | 4 | AAB47087 Anti-IGE |
| 6 | 596 | 100.0 | 218 | 4 | AAB76949 Full leng |
| 7 | 596 | 100.0 | 218 | 4 | AAB76951 Full leng |
| 8 | 596 | 100.0 | 218 | 4 | AAB76953 Variable |
| 9 | 596 | 100.0 | 218 | 4 | AAB76958 Variable |
| 10 | 596 | 100.0 | 218 | 8 | ADN07045 Anti-IGE |
| 11 | 596 | 100.0 | 218 | 8 | ADN07036 Anti-IGE |
| 12 | 596 | 100.0 | 218 | 8 | ADN07038 Anti-IGE |
| 13 | 596 | 100.0 | 218 | 8 | ADN07040 Anti-IGE |
| 14 | 594 | 99.7 | 114 | 2 | AAW95653 Mus muscu |
| 15 | 594 | 99.7 | 218 | 2 | AAW95660 Mus muscu |
| 16 | 594 | 99.7 | 218 | 2 | AAW95662 Mus muscu |
| 17 | 594 | 99.7 | 218 | 2 | AAV50030 Human E27 |
| 18 | 594 | 99.7 | 218 | 3 | AAB07472 Amino aci |
| 19 | 594 | 99.7 | 218 | 4 | AAB74211 E27 anti- |
| 20 | 594 | 99.7 | 218 | 6 | ABU62797 E27 anti- |
| 21 | 594 | 99.7 | 218 | 7 | ADP69597 Human ant |
| 22 | 594 | 99.7 | 218 | 7 | ADP29038 Anti-IGE |
| 23 | 587 | 98.5 | 248 | 2 | AAW95668 Mus muscu |
| 24 | 587 | 98.5 | 248 | 2 | AAW95667 Mus muscu |
| 25 | 587 | 98.5 | 248 | 4 | AAB76957 SfV fragm |

| | | | | | | |
|----|-----|------|-----|---|----------|--------------------|
| 26 | 587 | 98.5 | 248 | 4 | AAB76956 | Aab76956 SfV fragm |
| 27 | 587 | 98.5 | 248 | 8 | ADN07044 | Adn07044 Anti-IGE |
| 28 | 587 | 98.5 | 248 | 8 | ADN07043 | Adn07043 Anti-IGE |
| 29 | 575 | 96.5 | 114 | 4 | AAB76943 | Aab76943 Variable |
| 30 | 575 | 96.5 | 114 | 8 | ADN07030 | Adn07030 Anti-IGE |
| 31 | 575 | 96.5 | 219 | 8 | ADN07066 | Adn07066 F(ab)-pha |
| 32 | 573 | 96.1 | 114 | 2 | AAW95654 | Aaw95654 Mus muscu |
| 33 | 570 | 95.6 | 114 | 2 | AAW95655 | Aaw95655 Mus muscu |
| 34 | 570 | 95.6 | 114 | 4 | AAB76944 | Aab76944 Variable |
| 35 | 570 | 95.6 | 114 | 8 | ADN07031 | Adn07031 Anti-IGE |
| 36 | 570 | 95.6 | 218 | 2 | AAW95658 | Aaw95658 Mus muscu |
| 37 | 570 | 95.6 | 218 | 3 | AAW85200 | Aay85200 Light cha |
| 38 | 570 | 95.6 | 218 | 4 | AAB76947 | Aab76947 Full vari |
| 39 | 570 | 95.6 | 218 | 8 | ADN07034 | Adn07034 Anti-IGE |
| 40 | 570 | 95.6 | 241 | 8 | ADQ90719 | Adq90719 Anti-IGE |
| 41 | 570 | 95.6 | 241 | 8 | ADQ90717 | Adq90717 Anti-IGE |
| 42 | 563 | 94.5 | 218 | 2 | AAK33312 | Humanised |
| 43 | 556 | 93.3 | 111 | 2 | AAW95651 | Aaw95651 Mus muscu |
| 44 | 556 | 93.3 | 111 | 4 | AAB76940 | Aab76940 Variable |
| 45 | 556 | 93.3 | 111 | 8 | ADN07027 | Adn07027 Murine an |

ALIGNMENTS

RESULT 1
AAB76942
ID AAB76942 standard; protein; 114 AA.
XX
AC AAB76942;
XX
DT 17-APR-2001 (first entry)
XX
DE Variable light chain sequence of e26 and e27 SEQ ID 8.
XX
KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
KW conjunctivitis; eczema; urticaria; food allergy.
XX
OS Synthetic.
XX
PN US6172213-B1.
XX
PD 09-JAN-2001.
XX
PF 30-JUN-1998; 98US-00109207.
XX
PR 02-JUL-1997; 97US-0051554P.
XX
PA (GETH) GENENTECH INC.
XX
PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX
DR WPI; 2001-122353/13.
XX
PT New nucleic acid encoding anti-immunoglobulin E antibody with improved
PT properties, produced by substituting aspartyl residues in unimproved
PT immunoglobulin E prone to isomerization by other residues by affinity
PT maturation with phage display.
XX
PS Disclosure; Fig 2; 87pp; English.

This invention relates to a nucleotide sequence encoding an antibody with improved anti-IGE antibody activity. The antibody has improved action due to a process comprising, a) identifying aspartyl residues prone to isomerisation in unimproved anti-IGE (immunoglobulin E) antibody; b) substituting alternative residues to create candidate molecules; and c) selecting those candidate molecules which display affinity against the target molecule. Use of the antibody results in antiasthmatic; antiallergic; ophthalmological; dermatological and antiinflammatory activity. The antibodies are useful for treating IgE-mediated disorders such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and food allergies. The mutant antibodies produced by the above mentioned

CC nucleic acids may also be used as affinity purification agents and in
 CC diagnostic assays for detecting the expression of an antigen of interest
 CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
 CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
 CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
 CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
 CC used in the generation of affinity improved anti-IgE antibodies
 XX
 SQ Sequence 114 AA;

Query Match 100.0%; Score 596; DB 4; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.2e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGRVITTCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
 |||||
 Db 1 DIQLTQSPSSLSASVGRVITTCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
 |||||
 QY 61 GVPFRFSGSGSGDTFTLTISLQPEDPATYCCQSHEDPYTFGGTKVEIKRTV 114
 |||||
 Db 61 GVPFRFSGSGSGDTFTLTISLQPEDPATYCCQSHEDPYTFGGTKVEIKRTV 114

RESULT 2

ADN07029
 ID ADN07029 standard; protein; 114 AA.

AC ADN07029;

XX 01-JUL-2004 (first entry)

DE Anti-IgE antibody e26 and e27 variable light chain domain (VL).

XX Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
 KW therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
 KW allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
 KW variable light chain domain; VL.

XX Unidentified.

XX Key Location/Qualifiers
 FH Region 24..40
 FT /label= CDR-L1
 FT Region 54..60
 FT /label= CDR-L2
 FT Region 93..100
 FT /label= CDR-L3

XX US6723833-B1.

XX 20-APR-2004.

XX 17-NOV-2000; 2000US-00716028.

XX 02-JUL-1997; 97US-0051554P.

XX 30-JUN-1998; 98US-00109207.

XX (GETH) GENENTECH INC.

XX Lowman HB, Presta LG, Jardieu PM, Lowe J;

XX WPI; 2004-326922/30.

XX New composition of an improved anti-IgE antibody or IgE binding fragment,
 PT useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
 PT conjunctivitis, eczema, urticaria or food allergies.

XX Disclosure; SEQ ID NO 8; 89pp; English.

XX The invention relates to therapeutic compositions comprising anti-IgE
 CC antibody or IgE binding fragment in combination with an adjunct
 CC immunosuppressive agent. The composition is useful for treating IgE-
 CC mediated disorders. The disorders include atopic allergy associated with

CC anaphylactic hypersensitivity and asthma, allergic rhinitis and
 CC conjunctivitis, eczema, urticaria and food allergies. The present
 CC sequence is an anti-IgE antibody variable light chain domain (VL).
 XX
 SQ Sequence 114 AA;

Query Match 100.0%; Score 596; DB 8; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.2e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGRVITTCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
 |||||
 Db 1 DIQLTQSPSSLSASVGRVITTCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
 |||||

QY 61 GVPFRFSGSGSGDTFTLTISLQPEDPATYCCQSHEDPYTFGGTKVEIKRTV 114
 |||||
 Db 61 GVPFRFSGSGSGDTFTLTISLQPEDPATYCCQSHEDPYTFGGTKVEIKRTV 114

RESULT 3

AAW95664

ID AAW95664 standard; protein; 218 AA.

XX AAW95664;

XX 08-JUN-1999 (first entry)

DE Mus musculus anti-IgE e26 & e27 variable light chain Fab fragment.

XX Variable light Fab fragment; antibody; anti-IgE; reduction; prevention;
 KW histamine; production; hypersensitivity; allergen; anaphylaxis;
 KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
 KW eczema; anaphylactic shock; urticaria; IgE.

XX Mus musculus.

XX WO9901556-A2.

XX 14-JAN-1999.

XX 30-JUN-1998; 98WO-US013410.

XX 02-JUL-1997; 97US-00887352.

XX (GETH) GENENTECH INC.

XX Lowman HB, Presta LG, Jardieu PM, Lowe J;

XX WPI; 1999-106057/09.

XX Improving affinity of polypeptides, particularly anti-IgE antibodies - by
 PT identifying aspartyl residues which undergo isomerisation and
 PT substituting alternative residues and screening for affinity against the
 PT target.

XX Disclosure; Page 99-100; 129pp; English.

XX The sequence is that of the variable light Fab fragment of e26 and e27.
 CC It was used as part of a method to improve the affinity of anti-IgE
 CC antibodies such as e26 and e27. The e26 and e27 antibodies can be used
 CC for reducing or preventing IgE mediated production of histamine in a
 CC mammal. They can be used for treating a disorder mediated by IgE such as
 CC hypersensitivity, atopic allergy, asthma, allergic rhinitis,
 CC conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The
 CC antibodies can also be used for affinity purification, detection and
 CC diagnosis

XX Sequence 218 AA;

Query Match 100.0%; Score 596; DB 2; Length 218;
 Best Local Similarity 100.0%; Pred. No. 2.1e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASKPVDGSDSYLNWYQOKPGKAPKLLIYAASYLE 60
 Db 1 DIQLTQSPSSLSASVGDRTVITTCRASKPVDGSDSYLNWYQOKPGKAPKLLIYAASYLE 60

QY 61 GVPFRFSGSGSGTDFTLTISSLPQEDFATYTCQSHEDPYTFGQGTKEIKRTV 114
 Db 61 GVPFRFSGSGSGTDFTLTISSLPQEDFATYTCQSHEDPYTFGQGTKEIKRTV 114

RESULT 4
 AAW95669 ID AAW95669 standard; protein; 218 AA.
 XX AC AAW95669;
 XX DT 08-JUN-1999 (first entry)
 XX DE Mus musculus anti-IgE e26 & e27 variable light chain F(ab)'2 fragment.
 XX KW Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;
 XX KW histamine; production; hypersensitivity; allergen; anaphylaxis;
 XX KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
 XX KW eczema; anaphylactic shock; urticaria; F(ab)'2 fragment.
 XX OS Mus musculus.
 XX FN WO9901556-A2.
 XX PD 14-JAN-1999.
 XX PF 30-JUN-1998; 98WO-US013410.
 XX PR 02-JUL-1997; 97US-00887352.
 XX PA (GETH) GENENTECH INC.
 XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX WPI; 1999-106057/09.
 XX PT Improving affinity of polypeptides, particularly anti-IgE antibodies - by
 PT identifying aspartyl residues which undergo isomerisation and
 PT substituting alternative residues and screening for affinity against the
 PT target.
 XX PS Disclosure; Page 104; 129pp; English.
 XX CC The sequence is that of the variable light chain F(ab)'2 fragment of e26
 CC and e27. It was used as part of a method to improve the affinity of anti-
 CC IgE antibodies such as e26 and e27. The e26 and e27 antibodies can be
 CC used for reducing or preventing IgE mediated production of histamine in a
 CC mammal. They can be used for treating a disorder mediated by IgE such as
 CC hypersensitivity, atopic allergy, asthma, allergic rhinitis,
 CC conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The
 CC antibodies can also be used for affinity purification, detection and
 CC diagnosis
 XX SQ Sequence 218 AA;
 Query Match 100.0%; Score 596; DB 2; Length 218;
 Best Local Similarity 100.0%; Pred. No. 2.1e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASKPVDGSDSYLNWYQOKPGKAPKLLIYAASYLE 60
 Db 1 DIQLTQSPSSLSASVGDRTVITTCRASKPVDGSDSYLNWYQOKPGKAPKLLIYAASYLE 60

QY 61 GVPFRFSGSGSGTDFTLTISSLPQEDFATYTCQSHEDPYTFGQGTKEIKRTV 114
 Db 61 GVPFRFSGSGSGTDFTLTISSLPQEDFATYTCQSHEDPYTFGQGTKEIKRTV 114

RESULT 5
 AAW76949 ID AAW76949 standard; protein; 218 AA.
 XX AC AAW76949;

AAB47087
 ID AAB47087 standard; protein; 218 AA.
 XX AC AAB47087;
 XX DT 11-SEP-2003 (revised)
 XX DT 08-MAY-2001 (first entry)
 XX DE Anti-IgE antibody, E26, light chain.
 XX KW Light chain; heavy chain; anti-IgE antibody; E26; transfection;
 XX KW green fluorescent protein; GFP; promoter; expression.
 XX OS Homo sapiens.
 XX OS Mus musculus.
 XX OS Chimeric.
 XX PN WO200104306-A1.
 XX PD 18-JAN-2001.
 XX PF 11-JUL-2000; 2000WO-US018841.
 XX PR 12-JUL-1999; 99US-0143360P.
 XX PA (GETH) GENENTECH INC.
 XX PI Chisholm V, Crowley CW, Krummen LA, Meng YG;
 XX WPI; 2001-138352/14.
 XX PT Novel polynucleotide construct for screening and obtaining cells
 PT expressing high levels of desired protein, comprises amplifiable
 PT selectable gene, fluorescent protein gene and sequence encoding desired
 PT product.
 XX PS Disclosure; Fig 13A; 75pp; English.
 XX CC The sequences given in AAB47087-88 represent the light and heavy chains
 CC of the anti-IgE antibody, E26. These sequences were expressed by the
 CC construct of the invention, which comprises an amplifiable selectable
 CC gene, a green fluorescent protein gene (GFP), and a selected sequence
 CC encoding a desired product, which is operably linked to either the
 CC amplifiable selectable gene or to the GFP gene, and to a promoter.
 CC Constructs such as this, are useful for producing a desired product by
 CC introduction into a suitable eukaryotic cell, culturing the resultant
 CC eukaryotic cell under conditions so as to express the desired product,
 CC and recovering the desired product from the culture medium. The
 CC constructs are efficient for identifying and selecting for stable
 CC eukaryotic cells expressing high levels of a desired product. They are
 CC suitable for earlier and faster screening of transfected cells. (Updated
 CC on 11-SEP-2003 to standardise OS field)
 XX SQ Sequence 218 AA;
 Query Match 100.0%; Score 596; DB 4; Length 218;
 Best Local Similarity 100.0%; Pred. No. 2.1e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASKPVDGSDSYLNWYQOKPGKAPKLLIYAASYLE 60
 Db 1 DIQLTQSPSSLSASVGDRTVITTCRASKPVDGSDSYLNWYQOKPGKAPKLLIYAASYLE 60

QY 61 GVPFRFSGSGSGTDFTLTISSLPQEDFATYTCQSHEDPYTFGQGTKEIKRTV 114
 Db 61 GVPFRFSGSGSGTDFTLTISSLPQEDFATYTCQSHEDPYTFGQGTKEIKRTV 114

RESULT 6
 AAB76949 ID AAB76949 standard; protein; 218 AA.
 XX AC AAB76949;

XX 17-APR-2001 (first entry)
 XX Full length light chain sequence of e26 SEQ ID 15.
 DE Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
 XX antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
 KW conjunctivitis; eczema; urticaria; food allergy.
 KW Synthetic.
 OS US6172213-B1.
 XX 09-JAN-2001.
 XX 30-JUN-1998; 98US-00109207.
 XX 02-JUL-1997; 97US-0051554P.
 XX (GETH) GENENTECH INC.
 XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX WPI; 2001-122353/13.
 XX New nucleic acid encoding anti-immunoglobulin E antibody with improved
 PT properties, produced by substituting aspartyl residues in unimproved
 PT immunoglobulin E prone to isomerization by other residues by affinity
 PT maturation with phage display.
 XX Claim 2; Fig 12; 87pp; English.
 XX This invention relates to a nucleotide sequence encoding an antibody with
 CC improved anti-IgE antibody activity. The antibody has improved action due
 CC to a process comprising, a) identifying aspartyl residues prone to
 CC isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
 CC substituting alternative residues to create candidate molecules; and c)
 CC selecting those candidate molecules which display affinity against the
 CC target molecule. Use of the antibody results in antiasthmatic;
 CC antiallergic; ophthalmological; dermatological and antiinflammatory
 CC activity. The antibodies are useful for treating IgE-mediated disorders
 CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
 CC food allergies. The mutant antibodies produced by the above mentioned
 CC nucleic acids may also be used as affinity purification agents and in
 CC diagnostic assays for detecting the expression of an antigen of interest
 CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
 CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
 CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
 CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
 CC used in the generation of affinity improved anti-IgE antibodies
 XX Sequence 218 AA;
 SQ Query Match 100.0%; Score 596; DB 4; Length 218;
 Best Local Similarity 100.0%; Pred. No. 2.1e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSLASVGRVITTCRASPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSLASVGRVITTCRASPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
 QY 61 GVPSRFGSGSGDTFTLTISLQPEDPATYCCQSHEDPTFFGGTKVEIKRTV 114
 DB 61 GVPSRFGSGSGDTFTLTISLQPEDPATYCCQSHEDPTFFGGTKVEIKRTV 114
 RESULT 7
 AAB76951
 ID AAB76951 standard; protein; 218 AA.
 XX AAB76951;
 AC AAB76951;
 DT 17-APR-2001 (first entry)

XX Full length light chain sequence of e27 SEQ ID 17.
 DE Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
 KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
 KW conjunctivitis; eczema; urticaria; food allergy.
 OS Synthetic.
 XX US6172213-B1.
 XX 09-JAN-2001.
 XX 30-JUN-1998; 98US-00109207.
 XX 02-JUL-1997; 97US-0051554P.
 XX (GETH) GENENTECH INC.
 XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX WPI; 2001-122353/13.
 XX New nucleic acid encoding anti-immunoglobulin E antibody with improved
 PT properties, produced by substituting aspartyl residues in unimproved
 PT immunoglobulin E prone to isomerization by other residues by affinity
 PT maturation with phage display.
 XX Claim 4; Fig 12; 87pp; English.
 XX This invention relates to a nucleotide sequence encoding an antibody with
 CC improved anti-IgE antibody activity. The antibody has improved action due
 CC to a process comprising, a) identifying aspartyl residues prone to
 CC isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
 CC substituting alternative residues to create candidate molecules; and c)
 CC selecting those candidate molecules which display affinity against the
 CC target molecule. Use of the antibody results in antiasthmatic;
 CC antiallergic; ophthalmological; dermatological and antiinflammatory
 CC activity. The antibodies are useful for treating IgE-mediated disorders
 CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
 CC food allergies. The mutant antibodies produced by the above mentioned
 CC nucleic acids may also be used as affinity purification agents and in
 CC diagnostic assays for detecting the expression of an antigen of interest
 CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
 CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
 CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
 CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
 CC used in the generation of affinity improved anti-IgE antibodies
 XX Sequence 218 AA;
 SQ Query Match 100.0%; Score 596; DB 4; Length 218;
 Best Local Similarity 100.0%; Pred. No. 2.1e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSLASVGRVITTCRASPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSLASVGRVITTCRASPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
 QY 61 GVPSRFGSGSGDTFTLTISLQPEDPATYCCQSHEDPTFFGGTKVEIKRTV 114
 DB 61 GVPSRFGSGSGDTFTLTISLQPEDPATYCCQSHEDPTFFGGTKVEIKRTV 114
 RESULT 8
 AAB76953
 ID AAB76953 standard; protein; 218 AA.
 XX AAB76953;
 AC AAB76953;
 DT 17-APR-2001 (first entry)
 DE Variable light chain Fab fragment of e26 and e27 SEQ ID 19.

XX Antibody; antiaesthematic; antiallergic; ophthalmological; dermatological;
 KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
 KW conjunctivitis; eczema; urticaria; food allergy.
 XX Synthetic.
 OS US6172213-B1.
 XX 09-JAN-2001.
 XX 30-JUN-1998; 98US-00109207.
 XX 02-JUL-1997; 97US-0051554P.
 XX (GETH) GENENTECH INC.
 XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX WPI; 2001-122353/13.
 XX New nucleic acid encoding anti-immunoglobulin E antibody with improved
 PT properties, produced by substituting aspartyl residues in unimproved
 PT immunoglobulin E prone to isomerization by other residues by affinity
 PT maturation with phage display.
 XX Claim 1; Fig 13; 87pp; English.
 XX This invention relates to a nucleotide sequence encoding an antibody with
 CC improved anti-IgE antibody activity. The antibody has improved action due
 CC to a process comprising, a) identifying aspartyl residues prone to
 CC isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
 CC substituting alternative residues to create candidate molecules, and c)
 CC selecting those candidate molecules which display affinity against the
 CC target molecule. Use of the antibody results in antiasthmatic;
 CC antiallergic; ophthalmological; dermatological and antiinflammatory
 CC activity. The antibodies are useful for treating IgE-mediated disorders
 CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
 CC food allergies. The mutant antibodies produced by the above mentioned
 CC nucleic acids may also be used as affinity purification agents and in
 CC diagnostic assays for detecting the expression of an antigen of interest
 CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
 CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
 CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
 CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
 CC used in the generation of affinity improved anti-IgE antibodies
 XX SQ Sequence 218 AA;
 Query Match 100.0%; Score 596; DB 4; Length 218;
 Best Local Similarity 100.0%; Pred. No. 2.1e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQLTQSPSSLASVGRVTITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 60
 Db 1 DIQLTQSPSSLASVGRVTITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 60
 Qy 61 GVPFRFGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGQTKVEIKRTV 114
 Db 61 GVPFRFGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGQTKVEIKRTV 114
 RESULT 9
 AAB76958
 ID AAB76958 standard; protein; 218 AA.
 XX AC AAB76958;
 XX 17-APR-2001 (first entry)
 XX Variable light chain F(ab)'2 fragment of e26 and e27 SEQ ID 24.
 DE Antibody; antiaesthematic; antiallergic; ophthalmological; dermatological;

KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
 KW conjunctivitis; eczema; urticaria; food allergy.
 XX Synthetic.
 OS US6172213-B1.
 XX 09-JAN-2001.
 XX 30-JUN-1998; 98US-00109207.
 XX 02-JUL-1997; 97US-0051554P.
 XX (GETH) GENENTECH INC.
 XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX WPI; 2001-122353/13.
 XX New nucleic acid encoding anti-immunoglobulin E antibody with improved
 PT properties, produced by substituting aspartyl residues in unimproved
 PT immunoglobulin E prone to isomerization by other residues by affinity
 PT maturation with phage display.
 XX Claim 1; Fig 15; 87pp; English.
 XX This invention relates to a nucleotide sequence encoding an antibody with
 CC improved anti-IgE antibody activity. The antibody has improved action due
 CC to a process comprising, a) identifying aspartyl residues prone to
 CC isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
 CC substituting alternative residues to create candidate molecules, and c)
 CC selecting those candidate molecules which display affinity against the
 CC target molecule. Use of the antibody results in antiasthmatic;
 CC antiallergic; ophthalmological; dermatological and antiinflammatory
 CC activity. The antibodies are useful for treating IgE-mediated disorders
 CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
 CC food allergies. The mutant antibodies produced by the above mentioned
 CC nucleic acids may also be used as affinity purification agents and in
 CC diagnostic assays for detecting the expression of an antigen of interest
 CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
 CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
 CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
 CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
 CC used in the generation of affinity improved anti-IgE antibodies
 XX SQ Sequence 218 AA;
 Query Match 100.0%; Score 596; DB 4; Length 218;
 Best Local Similarity 100.0%; Pred. No. 2.1e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DIQLTQSPSSLASVGRVTITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 60
 Db 1 DIQLTQSPSSLASVGRVTITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 60
 Qy 61 GVPFRFGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGQTKVEIKRTV 114
 Db 61 GVPFRFGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGQTKVEIKRTV 114
 RESULT 10
 ADN07045
 ID ADN07045 standard; protein; 218 AA.
 XX AC ADN07045;
 XX 01-JUL-2004 (first entry)
 XX Anti-IgE antibody e26 and e27 variable light (VL) F(ab)' 2 fragment.
 DE Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
 KW therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
 KW allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;

KW variable light chain; VL.
 OS Unidentified.
 XX US6723833-B1.
 PN 20-APR-2004.
 XX 17-NOV-2000; 2000US-00716028.
 XX 02-JUL-1997; 97US-0051554P.
 PR 30-JUN-1998; 98US-00109207.
 XX (GETH) GENENTECH INC.
 PA Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX WPI; 2004-326922/30.
 XX New composition of an improved anti-IgE antibody or IgE binding fragment,
 XX useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
 XX conjunctivitis, eczema, urticaria or food allergies.
 XX Claim 7; SEQ ID NO 24; 89pp; English.
 PS The invention relates to therapeutic compositions comprising anti-IgE
 CC antibody or IgE binding fragment in combination with an adjunct
 CC immunosuppressive agent. The composition is useful for treating IgE-
 CC mediated disorders. The disorders include atopic allergy associated with
 CC anaphylactic hypersensitivity and asthma, allergic rhinitis and
 CC conjunctivitis, eczema, urticaria and food allergies. The present
 CC sequence is an anti-IgE antibody variable light chain (VL) F(ab)' 2
 CC fragment.
 XX Sequence 218 AA;
 SQ

Query Match 100.0%; Score 596; DB 8; Length 218;
 Best Local Similarity 100.0%; Pred. No. 2.1e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSSLASVGRVTITCRASKPVDGEGSYLNWYQQKPGKAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSSLASVGRVTITCRASKPVDGEGSYLNWYQQKPGKAPKLLIYAASYLE 60
 QY 61 GVPSRFGSGSGTDFLTITSSLPQEDPATYVYCOQSHEDPYTFGGTKVEIKRTV 114
 DB 61 GVPSRFGSGSGTDFLTITSSLPQEDPATYVYCOQSHEDPYTFGGTKVEIKRTV 114

RESULT 11
 ADN07036
 ID ADN07036 standard; protein; 218 AA.
 AC ADN07036;
 XX 01-JUL-2004 (first entry)
 DT Anti-IgE antibody e26 full length variable light chain (VL).
 DE Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
 KW therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
 KW allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
 KW variable light chain; VL.
 XX Unidentified.
 OS US6723833-B1.
 XX 20-APR-2004.
 XX 17-NOV-2000; 2000US-00716028.
 XX 02-JUL-1997; 97US-0051554P.
 PR 30-JUN-1998; 98US-00109207.
 XX (GETH) GENENTECH INC.
 PA Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX WPI; 2004-326922/30.
 XX New composition of an improved anti-IgE antibody or IgE binding fragment,
 XX useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
 XX conjunctivitis, eczema, urticaria or food allergies.

PR 30-JUN-1998; 98US-00109207.
 XX (GETH) GENENTECH INC.
 PA Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX WPI; 2004-326922/30.
 XX New composition of an improved anti-IgE antibody or IgE binding fragment,
 XX useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
 XX conjunctivitis, eczema, urticaria or food allergies.
 XX Claim 1; SEQ ID NO 15; 89pp; English.
 PS The invention relates to therapeutic compositions comprising anti-IgE
 CC antibody or IgE binding fragment in combination with an adjunct
 CC immunosuppressive agent. The composition is useful for treating IgE-
 CC mediated disorders. The disorders include atopic allergy associated with
 CC anaphylactic hypersensitivity and asthma, allergic rhinitis and
 CC conjunctivitis, eczema, urticaria and food allergies. The present
 CC sequence is an anti-IgE antibody variable light chain (VL).
 XX Sequence 218 AA;
 SQ

Query Match 100.0%; Score 596; DB 8; Length 218;
 Best Local Similarity 100.0%; Pred. No. 2.1e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSSLASVGRVTITCRASKPVDGEGSYLNWYQQKPGKAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSSLASVGRVTITCRASKPVDGEGSYLNWYQQKPGKAPKLLIYAASYLE 60
 QY 61 GVPSRFGSGSGTDFLTITSSLPQEDPATYVYCOQSHEDPYTFGGTKVEIKRTV 114
 DB 61 GVPSRFGSGSGTDFLTITSSLPQEDPATYVYCOQSHEDPYTFGGTKVEIKRTV 114

RESULT 12
 ADN07038
 ID ADN07038 standard; protein; 218 AA.
 AC ADN07038;
 XX 01-JUL-2004 (first entry)
 DT Anti-IgE antibody e27 full length variable light chain (VL).
 DE Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
 KW therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
 KW allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
 KW variable light chain; VL.
 XX Unidentified.
 OS US6723833-B1.
 XX 20-APR-2004.
 XX 17-NOV-2000; 2000US-00716028.
 XX 02-JUL-1997; 97US-0051554P.
 PR 30-JUN-1998; 98US-00109207.
 XX (GETH) GENENTECH INC.
 PA Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX WPI; 2004-326922/30.
 XX New composition of an improved anti-IgE antibody or IgE binding fragment,
 XX useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
 XX conjunctivitis, eczema, urticaria or food allergies.

PS Claim 1; SEQ ID NO 17; 89pp; English.

XX The invention relates to therapeutic compositions comprising anti-IgE antibody or IgE binding fragment in combination with an adjunct immunosuppressive agent. The composition is useful for treating IgE-mediated disorders. The disorders include atopic allergy associated with anaphylactic hypersensitivity and asthma, allergic rhinitis and conjunctivitis, eczema, urticaria and food allergies. The present sequence is an anti-IgE antibody variable light chain (VL).

XX SQ Sequence 218 AA;

Query Match 100.0%; Score 596; DB 8; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.1e-35;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQOKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQOKPGKAPKLLIYAASYLE 60

Qy 61 GVPFRFSGSGGTDTLTITSSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
Db 61 GVPFRFSGSGGTDTLTITSSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTV 114

RESULT 13

ADN07040

ID ADN07040 standard; protein; 218 AA.

AC ADN07040;

XX 01-JUL-2004 (first entry)

XX Anti-IgE antibody e26 and e27 variable light (VL) Fab fragment.

XX Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder; therapy; atopic allergy; anaphylactic hypersensitivity; asthma; allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy; variable light chain; VL.

XX OS Unidentified.

XX US6723833-B1.

XX 20-APR-2004.

XX 17-NOV-2000; 2000US-00716028.

XX 02-JUL-1997; 97US-0051554P.

XX 30-JUN-1998; 98US-00109207.

XX (GETH) GENENTECH INC.

XX Lowman HB, Presta LG, Jardieu PM, Lowe J;

XX WPI; 2004-326922/30.

XX New composition of an improved anti-IgE antibody or IgE binding fragment, useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma, conjunctivitis, eczema, urticaria or food allergies.

XX Claim 7; SEQ ID NO 19; 89pp; English.

XX The invention relates to therapeutic compositions comprising anti-IgE antibody or IgE binding fragment in combination with an adjunct immunosuppressive agent. The composition is useful for treating IgE-mediated disorders. The disorders include atopic allergy associated with anaphylactic hypersensitivity and asthma, allergic rhinitis and conjunctivitis, eczema, urticaria and food allergies. The present sequence is an anti-IgE antibody variable light chain (VL) Fab fragment.

XX SQ Sequence 218 AA;

Query Match 100.0%; Score 596; DB 8; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.1e-35;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQOKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQOKPGKAPKLLIYAASYLE 60

Qy 61 GVPFRFSGSGGTDTLTITSSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
Db 61 GVPFRFSGSGGTDTLTITSSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTV 114

RESULT 14

AAW95653

ID AAW95653 standard; protein; 114 AA.

AC AAW95653;

XX 08-JUN-1999 (first entry)

XX Mus musculus anti-IgE e26 & e27 variable light chain.

XX Variable light chain; IgE; antibody; anti-IgE; reduction; prevention; histamine; production; hypersensitivity; allergen; anaphylaxis; atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever; eczema; anaphylactic shock; urticaria.

XX OS Mus musculus.

XX WO9901556-A2.

XX 14-JAN-1999.

XX 30-JUN-1998; 98WO-US013410.

XX 02-JUL-1997; 97US-00887352.

XX (GETH) GENENTECH INC.

XX Lowman HB, Presta LG, Jardieu PM, Lowe J;

XX WPI; 1999-106057/09.

XX Improving affinity of polypeptides, particularly anti-IgE antibodies - by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the target.

XX Disclosure; Page 89; 129pp; English.

XX The sequence is that of the variable light chain of e26 and e27. It was used as part of a method to improve the affinity of anti-IgE antibodies such as e26 and e27. The e26 and e27 antibodies can be used for reducing or preventing IgE mediated production of histamine in a mammal. They can be used for treating a disorder mediated by IgE such as hypersensitivity, atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The antibodies can also be used for affinity purification, detection and diagnosis

XX SQ Sequence 114 AA;

Query Match 99.7%; Score 594; DB 2; Length 114;
Best Local Similarity 99.1%; Pred. No. 1.6e-35;
Matches 113; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQOKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQOKPGKAPKLLIYAASYLE 60

Qy 61 GVPFRFSGSGGTDTLTITSSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
Db 61 GVPFRFSGSGGTDTLTITSSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTV 114

Search completed: June 3, 2005, 09:09:07
Job time : 38.3502 secs

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OM protein - protein search, using sw model

Run on: June 3, 2005, 08:53:28 ; Search time 7.09576 Seconds
(without alignments)
1545.812 Million cell updates/sec

Title: US-10-791-619-11

Perfect score: 623

Sequence: 1 EVQLVESGGGLVQPGGSLRL.....YCARGSHYFGHWFAVWGQG 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 419 | 67.3 | 140 | 2 S31588 | Ig heavy chain V r |
| 2 | 418.5 | 67.2 | 140 | 2 S70442 | Ig heavy chain pre |
| 3 | 418 | 67.1 | 123 | 2 S31114 | Ig heavy chain - h |
| 4 | 416 | 66.8 | 138 | 2 S31666 | Ig heavy chain V r |
| 5 | 413 | 66.3 | 121 | 2 S31113 | Ig heavy chain - h |
| 6 | 411.5 | 66.1 | 147 | 2 I37780 | Ig variable region |
| 7 | 409.5 | 65.7 | 122 | 2 E36005 | Ig heavy chain V r |
| 8 | 409.5 | 65.7 | 128 | 2 S48797 | Ig heavy chain V r |
| 9 | 409.5 | 65.7 | 141 | 2 S31669 | Ig heavy chain V r |
| 10 | 408 | 65.5 | 125 | 2 S30531 | Ig heavy chain V r |
| 11 | 407 | 65.3 | 117 | 2 S36259 | Ig heavy chain V r |
| 12 | 407 | 65.3 | 119 | 2 S31107 | Ig heavy chain - h |
| 13 | 404.5 | 64.9 | 122 | 2 S31117 | Ig heavy chain - h |
| 14 | 404 | 64.8 | 121 | 2 S19666 | Ig heavy chain V r |
| 15 | 404 | 64.8 | 121 | 2 E36005 | Ig heavy chain V r |
| 16 | 404 | 64.8 | 135 | 2 S31598 | Ig heavy chain V r |
| 17 | 404 | 64.8 | 140 | 2 S31686 | Ig heavy chain V r |
| 18 | 403 | 64.7 | 137 | 2 S38489 | Ig heavy chain V r |
| 19 | 401.5 | 64.4 | 137 | 2 S31701 | Ig heavy chain - h |
| 20 | 401 | 64.4 | 123 | 2 S26794 | Ig heavy chain V r |
| 21 | 400.5 | 64.3 | 124 | 2 S20782 | Ig heavy chain V r |
| 22 | 399.5 | 64.1 | 114 | 2 S36280 | Ig heavy chain V r |
| 23 | 399.5 | 64.1 | 136 | 2 S31587 | Ig heavy chain V r |
| 24 | 399 | 64.0 | 119 | 2 S31108 | Ig heavy chain - h |
| 25 | 399 | 64.0 | 160 | 2 S05271 | Ig heavy chain pre |
| 26 | 398 | 63.9 | 119 | 2 E36005 | Ig heavy chain V r |
| 27 | 398 | 63.9 | 143 | 2 S23624 | Ig heavy chain V r |
| 28 | 397 | 63.7 | 132 | 2 S31603 | Ig heavy chain V r |
| 29 | 396.5 | 63.6 | 116 | 2 S31110 | Ig heavy chain - h |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 396 | 63.6 | 120 | 1 M3HUBW | Ig heavy chain V-I |
| 31 | 396 | 63.6 | 130 | 2 S31601 | Ig heavy chain V r |
| 32 | 396 | 63.6 | 139 | 2 I37781 | Ig variable region |
| 33 | 395.5 | 63.5 | 118 | 2 S31116 | Ig heavy chain - h |
| 34 | 395.5 | 63.5 | 120 | 2 S48798 | Ig heavy chain V r |
| 35 | 395.5 | 63.5 | 139 | 2 S31674 | Ig heavy chain V r |
| 36 | 395 | 63.4 | 119 | 2 C36005 | Ig heavy chain V r |
| 37 | 395 | 63.4 | 121 | 2 I55673 | Ig heavy chain - h |
| 38 | 395 | 63.4 | 134 | 2 S31699 | Ig heavy chain V r |
| 39 | 394.5 | 63.3 | 114 | 2 S46390 | Ig heavy chain V r |
| 40 | 394.5 | 63.3 | 122 | 2 PC2398 | anti-tetanus toxin |
| 41 | 394 | 63.2 | 119 | 2 F36005 | Ig heavy chain V r |
| 42 | 394 | 63.2 | 134 | 2 S31679 | Ig heavy chain V r |
| 43 | 393.5 | 63.2 | 122 | 1 M3HUM | Ig heavy chain V-I |
| 44 | 393.5 | 63.2 | 128 | 2 S26790 | Ig heavy chain V r |
| 45 | 393 | 63.1 | 117 | 2 S78486 | Ig heavy chain V r |

ALIGNMENTS

RESULT 1

S31588

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31588

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31588

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-140 <CUI>

A:Cross-references: EMBL:Z14200; NID:G30957; PIDN:CAA78569.1; PID:G30958

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 419; DB 2; Length 140;

Best Local Similarity 71.3%; Pred. No. 2.5e-30;

Matches 82; Conservative 12; Mismatches 19; Indels 2; Gaps 2;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAIVGYSITSGYSNNWIRQAPGKLEWASIKYS-GETK 59

Db 20 EVQLLESQGLVQPGGSLRLSCAIVGYSITSGYSNNWIRQAPGKLEWASIKYS-GETK 78

Qy 60 YNPVSKGRTITSRDSDKNTFYLMNSLRADTAVYVCARGSHYFGHWFAVWGQG 114

Db 79 YADSVKGRFTISRDDSKNTLYLMNSLRADTAVYVCARGSHYFGHWFAVWGQG 133

RESULT 2

S70442

Ig heavy chain precursor V region (mu) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C:Accession: S70442

R:Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelles, C.

Mol. Immunol. 29, 1363-1373, 1992

A>Title: IGM kappa/lambda BBV human B cell clone: an early step of differentiation of fet

A:Reference number: S70442; MUID:93024508; PMID:1383695

A:Accession: S70442

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-140 <CUI>

A:Cross-references: UNIPROT:Q8WUK1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.2%; Score 418.5; DB 2; Length 140;

Best Local Similarity 72.2%; Pred. No. 2.7e-30;

| | | | | | | | | | |
|-----------------------------------------------|------------------------------------------------------------------------------------|-----------------------------|---------------------------------------|-----------------------|-----------------|----------|--------|------|----|
| Matches | 83; | Conservative | 9; | Mismatches | 20; | Indels | 3; | Gaps | 3; |
| QY | 1 | EVQLVESGGGLVQP...GSLRLSCA | VSGYSITSGYSNWNRQA | PQGKLEWVASIKYSGETK-59 | : | : :: : | :: : | : | : |
| Db | 20 | QVQLVESGGGVLP...GGSLRLS | CAASGFTF-SNYGMHWVRQA | PGKLEWAFIRYDGSNKY78 | : | : :: : | :: : | : | : |
| QY | 60 | YNPVSVKGRITISRDSDSKNTFYLQN | SIRADDTAVYYCARGSHYFGHHFAVMWGQ114 | : | : :: : | :: : | : | : | : |
| Db | 79 | YADVSVKGRFTISRDN SKNTLYLQNW | SIRADDTAVYYCAR-DHIVGATPYDWYGQ132 | : | : :: : | :: : | : | : | : |
| RESULT 3 | | | | | | | | | |
| S31114 | | | | | | | | | |
| C;Species: | Homo sapiens | (man) | | | | | | | |
| C;Date: | 02-Dec-1993 | #sequence_revision | 26-May-1995 | #text_change | 17-Mar-1999 | | | | |
| C;Accession: | S31114 | | | | | | | | |
| R;Raaphorst, | F.M.; Timmers, | E.; Kenter, | M.J.H.; van Tol, | M.J.D.; Vossen, | J.M.; Schuurman | | | | |
| Eur. J. Immunol. | 22, 247-251, | 1992 | | | | | | | |
| A;Title: | Restricted utilization of germ-line V(H)3 genes and short diverse third complement | | | | | | | | |
| A;Reference number: | S31104; | MUID: | 92111633; | PMID: | 1730252 | | | | |
| A;Accession: | S31114 | | | | | | | | |
| A;Status: | preliminary; | nucleic acid sequence | not shown; | translation | not shown | | | | |
| A:Molecule type: | mRNA | | | | | | | | |
| A;Residues: | 1-123 <RAA> | | | | | | | | |
| A;Note: | the nucleotide sequence was submitted to the EMBL Data Library, October 1991 | | | | | | | | |
| C;Superfamily: | immunoglobulin V region; | immunoglobulin homology | | | | | | | |
| C;Keywords: | heterotetramer; immunoglobulin | | | | | | | | |
| F;15-98/Domain: | immunoglobulin homology | <IMM> | | | | | | | |
| Query Match | 67.1%; | Score | 418; | DB 2; | Length | 123; | | | |
| Best Local Similarity | 71.8%; | Pred. No. | 2.7e+30; | | | | | | |
| Matches | 84; | Conservative | 11; | Mismatches | 18; | Indels | 4; | Gaps | 3; |
| QY | 1 | EVQLVESGGGLVQP...GSLRLSCA | VSGYSITSGYSNWNRQA | PQGKLEWVASIKYS-GETK59 | : | : :: : | :: : | : | : |
| Db | 1 | EVQLLES GGLVP...GGSLRLS | CAASGFTFS-YAMSWVRQA | PGKLEWSAISGSGSTY59 | : | : :: : | :: : | : | : |
| QY | 60 | YNPVSVKGRITISRDSDSKNTFYLQN | SIRADDTAVYYCARGSHY--FCWHHFVA VMWGQ114 | : | : :: : | :: : | : | : | : |
| Db | 60 | YADVSVKGRFTISRDN SKNTLYLQNW | SIRADDTAVYYCACASLYLRFLMLFDYWVGQ116 | : | : :: : | :: : | : | : | : |
| RESULT 4 | | | | | | | | | |
| S31666 | | | | | | | | | |
| Ig heavy chain V region - human (fragment) | | | | | | | | | |
| C;Species: | Homo sapiens | (man) | | | | | | | |
| C;Date: | 22-Nov-1993 | #sequence_revision | 10-Nov-1995 | #text_change | 23-Jul-1999 | | | | |
| C;Accession: | S31666 | | | | | | | | |
| R;Cuissinier, | A.M.; Gauthier, | L.; Boulbli, | L.; Fougereau, | M.; Tonnelle, | C. | | | | |
| submitted to the EMBL Data Library, June 1992 | | | | | | | | | |
| A;Description: | Mechanisms that generate human immunoglobulin diversity operate from the | | | | | | | | |
| A;Reference number: | S31585 | | | | | | | | |
| A;Accession: | S31666 | | | | | | | | |
| A;Status: | preliminary | | | | | | | | |
| A:Molecule type: | mRNA | | | | | | | | |
| A;Residues: | 1-138 <CUI> | | | | | | | | |
| A;Cross-references: | EMBL:Z14202; | NID:g30963; | PIDN:CAA78571.1; | PTD:g30964 | | | | | |
| C;Superfamily: | immunoglobulin V region; | immunoglobulin homology | | | | | | | |
| C;Keywords: | heterotetramer; immunoglobulin | | | | | | | | |
| F;34-117/Domain: | immunoglobulin homology | <IMM> | | | | | | | |
| Query Match | 66.8%; | Score | 416; | DB 2; | Length | 138; | | | |
| Best Local Similarity | 70.4%; | Pred. No. | 4.5e+30; | | | | | | |
| Matches | 81; | Conservative | 15; | Mismatches | 15; | Indels | 4; | Gaps | 3; |
| QY | 1 | EVQLVESGGGLVQP...GSLRLSCA | VSGYSITSGYSNWNRQA | PQGKLEWVASIKYS-GETK59 | : | : :: : | :: : | : | : |
| Db | 20 | EVQLLES GGLVP...GGSLRLS | CAASGFTFS-YAMSWVRQA | PGKLEWSAISGSGSTY78 | : | : :: : | :: : | : | : |
| QY | 60 | YNPVSVKGRITISRDSDSKNTFYLQN | SIRADDTAVYYCARGSHYFGHHFAVMWGQ114 | : | : :: : | :: : | : | : | : |


```
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; PMID:90349571; PMID:2117273
A:Accession: E36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <SCH>
A:Cross-references: GB:M34030
C:Genetics:
A:Gene: GDB:IGH@; IGHDI1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 65.7%; Score 409.5; DB 2; Length 122;
Best Local Similarity 70.1%; Pred. No. 1.5e-29;
Matches 82; Conservative 11; Mismatches 19; Indels 5; Gaps 4;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAGSITSGYSGYNNIRQAPGKGLWVASIKYSGTK- 59
Db 1 QVQLVESGGGVVQPGGSLRLSCAAGSITSGYSGYNNIRQAPGKGLWVASIVSYDGSNKY 59
Qy 60 YNPVSKGRITTSRDSSKNTFYLNQSLRAEDTAVYTCARGSHYFGHWAFA--VWGQ 114
Db 60 YADSVKGRFTISRDNKNTLYLNQSLRAEDTAVYTCARDRH--SSWYIGMDVWGQ 115

RESULT 8
S48797
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C:Accession: S48797; S26893
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S48797
A:Molecule type: mRNA
A:Residues: 1-128 <MAH>
A:Cross-references: EMBL:Z46379; NID:G587147; PIDN:CAA86512.1; PID:gl340168
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; PMID:93021117; PMID:1404388
A:Accession: S26893
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12350; NID:G32922; PIDN:CAA78220.1; PID:G32923
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 65.7%; Score 409.5; DB 2; Length 128;
Best Local Similarity 67.2%; Pred. No. 1.6e-29;
Matches 82; Conservative 15; Mismatches 16; Indels 9; Gaps 4;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAGSITSGYSGYNNIRQAPGKGLWVASIKYSGTK- 59
Db 1 QVQLVESGGGVVQPGGSLRLSCAAGSITSGYSGYNNIRQAPGKGLWVASIVSYDGSNKY 59
Qy 60 YNPVSKGRITTSRDSSKNTFYLNQSLRAEDTAVYTCARGSHYF---GHWF- ---AVWG 112
Db 60 YADSVKGRFTISRDNKNTLYLNQSLRAEDTAVYTCARDNYDSSGGYIYYGMDVWG 119
Qy 113 QG 114
Db 120 QG 121
```

```
RESULT 9
S31669
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31669
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31669
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-141 <CUI>
A:Cross-references: EMBL:Z14212; NID:G30959; PIDN:CAA78581.1; PID:G30960
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 65.7%; Score 409.5; DB 2; Length 141;
Best Local Similarity 70.7%; Pred. No. 1.7e-29;
Matches 82; Conservative 12; Mismatches 19; Indels 3; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAGSITSGYSGYNNIRQAPGKGLWVASIKYSGE-TK 59
Db 20 EVQLVESGGGLVQPGGSLRLSCAAGSITSGYSGYNNIRQAPGKGLWVASISSSSYIY 78
Qy 60 YNPVSKGRITTSRDSSKNTFYLNQSLRAEDTAVYTCARGSHYFGH-WHFAVWGQ 114
Db 79 YADSVKGRFTISRDNKNTLYLNQSLRAEDTAVYTCARGHRLTGEKGYFLWGRG 134

RESULT 10
S30531
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S30531
R:Mariette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30531
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-125 <MAR>
A:Cross-references: UNIPROT:Q9UL91; EMBL:Z18317
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 65.5%; Score 408; DB 2; Length 125;
Best Local Similarity 69.2%; Pred. No. 2.1e-29;
Matches 83; Conservative 11; Mismatches 18; Indels 8; Gaps 4;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAAGSITSGYSGYNNIRQAPGKGLWVASIKYGET-K 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAAGSITSGYSGYNNIRQAPGKGLWVASISSSSTIY 59
Qy 60 YNPVSKGRITTSRDSSKNTFYLNQSLRAEDTAVYTCAR-----GSHYFGHWHFAVWGQ 114
Db 60 YADSVKGRFTISRDNKNTLYLNQSLRAEDTAVYTCARSRNYDSSGYISH-YFDYWGQ 118

RESULT 11
S36259
Ig heavy chain V region (clone alpha-TNF-A1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36259
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; PMID:93178448; PMID:7679990
```

A;Accession: S36259
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-117 <GRI>
A;Cross-references: EMBL:Z18850; NID:g33123; PIDN:CAA79302.1; PID:g939902
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 65.3%; Score 407; DB 2; Length 117;
Best Local Similarity 68.6%; Pred. No. 2.4e-29;
Matches 81; Conservative 10; Mismatches 21; Indels 6; Gaps 3;

QY 1 EVLVESGGGLVQPGGSLRLSCAASGFTSS-YGMHWVRQAPGKLEWVAIFIRYDGSNKY 59
Db 1 EVLVESGGGLVQPGGSLRLSCAASGFTSS-YGMHWVRQAPGKLEWVAIFIRYDGSNKY 59

QY 60 YNPVSKGRITISRDSDSKNTFYLNLSRAEDTAVYVCARGSHYFGH-HFAVWGQ 113
Db 60 YADSVKGRFTISRDNKNTLYLNLSRAEDTAVYCVREDHVITTRGRVHYMDVWGK 117

RESULT 12
S31107
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31107
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Voessen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31107
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-119 <RAA>
A;Cross-references: EMBL:X62955
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 65.3%; Score 407; DB 2; Length 119;
Best Local Similarity 70.9%; Pred. No. 2.4e-29;
Matches 83; Conservative 12; Mismatches 14; Indels 8; Gaps 4;

QY 1 EVLVESGGGLVQPGGSLRLSCAASGFTSS-YAMSWVRQAPGKLEWVAISGSGSTY 59
Db 1 EVLVESGGGLVQPGGSLRLSCAASGFTSS-YAMSWVRQAPGKLEWVAISGSGSTY 59

QY 60 YNPVSKGRITISRDSDSKNTFYLNLSRAEDTAVYVCARGSHYFGH-HFAVWGQ 114
Db 60 YADSVKGRFTISRDNKNTLYLNLSRAEDTAVYCAKDPGASYY----FDYWGQG 112

RESULT 13
S31117
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31117
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Voessen, J.M.; Schuurman Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31117
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-122 <RAA>
A;Cross-references: EMBL:X62967
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 64.9%; Score 404.5; DB 2; Length 122;
Best Local Similarity 70.7%; Pred. No. 4.1e-29;
Matches 82; Conservative 9; Mismatches 22; Indels 3; Gaps 3;

QY 1 EVLVESGGGLVQPGGSLRLSCAASGFTSS-YGMHWVRQAPGKLEWVAISIKYSGETK- 59
Db 1 QVQLVSGGGVQPGGRSLRLSCAASGFTSS-YGMHWVRQAPGKLEWVAIVYDGSNKY 59

QY 60 YNPVSKGRITISRDSDSKNTFYLNLSRAEDTAVYVCARGSHYFGH-HFAVWGQ 114
Db 60 YADSVKGRFTISRDNKNTLYLNLSRAEDTAVYVCARDFFAPPNWSHFDYWGQ 115

RESULT 14
S19666
Ig heavy chain V region (VH3DJH4) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19666
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19666
A;Molecule type: mRNA
A;Residues: 1-121 <VAR>
A;Cross-references: EMBL:X61646; NID:g37688; PIDN:CAA43827.1; PID:g1333569
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 64.8%; Score 404; DB 2; Length 121;
Best Local Similarity 68.7%; Pred. No. 4.6e-29;
Matches 79; Conservative 12; Mismatches 22; Indels 2; Gaps 2;

QY 1 EVLVESGGGLVQPGGSLRLSCAASGFTSS-YGMHWVRQAPGKLEWVAISIKYSGETK- 59
Db 1 QVQLVSGGGVQPGGRSLRLSCAASGFTSS-YGMHWVRQAPGKLEWVAIVYDGSNKY 59

QY 60 YNPVSKGRITISRDSDSKNTFYLNLSRAEDTAVYVCARGSHYFGH-HFAVWGQ 114
Db 60 YADSVKGRFTISRDNKNTLYLNLSRAEDTAVYCAKTYSGSGWGYFDYWGQ 114

RESULT 15
G36005
Ig heavy chain V region (M74) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C;Accession: G36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:21117273
A;Accession: G36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
A;Cross-references: UNIPROT:Q8WUK1; GB:M34031
C;Genetics:
A;Gene: GDB:IGHD1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 64.8%; Score 404; DB 2; Length 121;
Best Local Similarity 70.4%; Pred. No. 4.6e-29;
Matches 81; Conservative 10; Mismatches 22; Indels 2; Gaps 2;

Search completed: June 3, 2005, 09:17:50
Job time : 7.09576 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 08:31:37 ; Search time 32.7497 Seconds
(without alignments)
1782.523 Million cell updates/sec

Title: US-10-791-619-11

Perfect score: 623

Sequence: 1 EVQLVESGGGLVQPGGSLRL.....YCARGSHYFGHHFAVWQG 114

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|------------|---------------------|
| 1 | 413 | 66.3 | 470 | 2 | Q6PJA4 | Q6pia4 homo sapien |
| 2 | 408 | 65.5 | 113 | 2 | Q9UL90 | Q9ul90 homo sapien |
| 3 | 399 | 64.0 | 466 | 2 | Q6IN78 | Q6in78 homo sapien |
| 4 | 398 | 63.9 | 478 | 2 | Q6PI81 | Q6pi81 homo sapien |
| 5 | 397.5 | 63.8 | 118 | 2 | Q9UL72 | Q9ul72 homo sapien |
| 6 | 396 | 63.6 | 120 | 1 | HV3E_HUMAN | P01766 homo sapien |
| 7 | 394.5 | 63.3 | 613 | 2 | Q8WUK1 | Q8wuk1 homo sapien |
| 8 | 394 | 63.2 | 240 | 2 | Q6SZC9 | Q6szc9 homo sapien |
| 9 | 394 | 63.2 | 472 | 2 | Q6N089 | Q6n089 homo sapien |
| 10 | 393.5 | 63.2 | 122 | 1 | HV3G_HUMAN | P01768 homo sapien |
| 11 | 392.5 | 63.0 | 118 | 2 | Q9UL91 | Q9ul91 homo sapien |
| 12 | 391.5 | 62.8 | 473 | 2 | Q6MZV7 | Q6mzv7 homo sapien |
| 13 | 391.5 | 62.8 | 606 | 2 | Q6GMY2 | Q6gmy2 homo sapien |
| 14 | 391 | 62.8 | 597 | 2 | Q96BB9 | Q96bb9 homo sapien |
| 15 | 389.5 | 62.5 | 475 | 2 | Q6MZQ6 | Q6mzq6 homo sapien |
| 16 | 389 | 62.4 | 116 | 2 | Q9UL93 | Q9ul93 homo sapien |
| 17 | 389 | 62.4 | 121 | 2 | Q9UL71 | Q9ul71 homo sapien |
| 18 | 389 | 62.4 | 464 | 2 | Q6MZU6 | Q6mzu6 homo sapien |
| 19 | 385 | 61.8 | 123 | 1 | HV24_MOUSE | P01793 mus musculus |
| 20 | 384.5 | 61.7 | 116 | 1 | HV05_CARAU | P19181 carassius a |
| 21 | 383.5 | 61.6 | 573 | 2 | Q8WU38 | Q8wu38 homo sapien |
| 22 | 382.5 | 61.4 | 147 | 2 | Q9Y509 | Q9y509 homo sapien |
| 23 | 382 | 61.3 | 117 | 1 | HV3C_HUMAN | P01764 homo sapien |
| 24 | 381 | 61.2 | 493 | 2 | Q6GMX2 | Q6gmx2 homo sapien |
| 25 | 380.5 | 61.1 | 494 | 2 | Q9EK68 | Q9ek68 homo sapien |
| 26 | 377.5 | 60.6 | 112 | 2 | Q9HCC1 | Q9hcc1 homo sapien |
| 27 | 377 | 60.5 | 493 | 2 | Q8NCL6 | Q8nc16 homo sapien |
| 28 | 374 | 60.0 | 115 | 1 | HV3F_HUMAN | P01767 homo sapien |
| 29 | 374 | 60.0 | 123 | 1 | HV22_MOUSE | P01791 mus musculus |
| 30 | 374 | 60.0 | 499 | 2 | Q8N5K4 | Q8n5k4 homo sapien |
| 31 | 372 | 59.7 | 119 | 1 | HV3I_HUMAN | P01770 homo sapien |

| | | | | | | |
|----|-------|------|-----|---|------------|---------------------|
| 32 | 371 | 59.6 | 487 | 2 | Q80Z17 | Q80zi7 mus musculus |
| 33 | 370 | 59.4 | 121 | 1 | HV3J_HUMAN | P01771 homo sapien |
| 34 | 369.5 | 59.3 | 122 | 1 | HV20_MOUSE | P01789 mus musculus |
| 35 | 368.5 | 59.1 | 479 | 2 | Q6MZV6 | Q6mzv6 homo sapien |
| 36 | 368.5 | 59.1 | 487 | 2 | Q6ZVX0 | Q6zvx0 homo sapien |
| 37 | 367 | 58.9 | 470 | 2 | Q7Z5W1 | Q7z5w1 homo sapien |
| 38 | 366.5 | 58.8 | 114 | 1 | HV3B_HUMAN | P01763 homo sapien |
| 39 | 366.5 | 58.8 | 122 | 1 | HV21_MOUSE | P01790 mus musculus |
| 40 | 366.5 | 58.8 | 487 | 2 | Q99KA4 | Q99ka4 mus musculus |
| 41 | 365 | 58.6 | 123 | 1 | HV18_MOUSE | P01787 mus musculus |
| 42 | 365 | 58.6 | 123 | 1 | HV23_MOUSE | P01792 mus musculus |
| 43 | 364 | 58.4 | 123 | 1 | HV19_MOUSE | P01788 mus musculus |
| 44 | 364 | 58.4 | 137 | 1 | HV46_MOUSE | P01822 mus musculus |
| 45 | 363 | 58.3 | 113 | 1 | HV30_MOUSE | P01799 mus musculus |

ALIGNMENTS

RESULT 1

Q6PJA4 PRELIMINARY; PRT; 470 AA.

AC Q6PJA4;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
EMBL; BC018747; AAH18747.1; -;
HSSP; P01861; IADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

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KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 66.3%; Score 413; DB 2; Length 470;
Best Local Similarity 72.4%; Pred. No. 1.2e-33;
Matches 84; Conservative 11; Mismatches 17; Indels 4; Gaps 4;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVGSYITSGYSNWIRQAPGKLEWVASIKYSGETKY 60
Db 20 EVQLVESGGGLVQPGGSLRLSCVVGTFSS-YWMSVVRQAPGKLEWVANIKDGSSEKY 78

Qy 61 N-PSVKGRITISRDDSKNTFYLNQNSLRADTAVYYCAR-GSHYFGHHFAVWGQG 114
Db 79 YDVSVKGRFTISRDNKNTLYLNQNSLRADTAVYYCARDSSWYRDW-FDPWGQG 133

RESULT 2
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035024; AAD56260.1; -.
DR PIR; S78486; S78486.
DR HSP; P01772; 2PB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 65.5%; Score 408; DB 2; Length 113;
Best Local Similarity 70.4%; Pred. No. 8.2e-34;
Matches 81; Conservative 10; Mismatches 14; Indels 10; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVGSYITSGYSNWIRQAPGKLEWVASIKYSGETK- 59
Db 1 EVQLVESGGGVQPGGSLRLSCAASGTFSS-YGMHVRQAPGKLEWVAFIRYDGSNKY 59

Qy 60 YNPSVKGRITISRDDSKNTFYLNQNSLRADTAVYYCARGSHYFGHHFAVWGQG 114
Db 60 YDVSVKGRFTISRDNKNTLYLNQNSLRADTAVYYCAKOLNY-----WGQG 106

RESULT 3
Q6IN78 PRELIMINARY; PRT; 466 AA.
ID Q6IN78;
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHL1 protein.
GN Name=IGHL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kzyvinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCDE81076E CRC64;

Query Match 64.0%; Score 399; DB 2; Length 466;
Best Local Similarity 69.3%; Pred. No. 3.2e-32;
Matches 79; Conservative 11; Mismatches 20; Indels 4; Gaps 2;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVGSYITSGYSNWIRQAPGKLEWVASIKYSGETKY 60
Db 20 EVQLVESGGGLIQPGGSLTSCAASGLTVSSNY-MHWVRQAPGKLEWVSVLYIGATYY 78

Qy 61 NPSVKGRITISRDDSKNTFYLNQNSLRADTAVYYCARGSHYFGHHFAVWGQG 114
Db 79 ADSVKGRFTISRDNKNTLYLNQNSLRADTAVYYCARGVYV---PAAPWGQG 129

RESULT 4
Q6PI81 PRELIMINARY; PRT; 478 AA.
ID Q6PI81;
AC Q6PI81;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozny K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
(2)
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 63.9%; Score 398; DB 2; Length 478;
Best Local Similarity 65.3%; Pred. No. 4.2e-32;
Matches 81; Conservative 15; Mismatches 16; Indels 12; Gaps 4;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 60
DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFS-YNMSWVRQAPGKLEWVANIKQDGSEKY 78

QY 61 N-PSVKGRTITSRDKNFTYLNMSLRADTAFTVYCAR-----GSHYFGHHFPAV 110
DB 79 YVDSVKGRTITSRDKNFTYLNMSLRADTAFTVYCARFEFSTTTVNADY-YFYMDV 137

QY 111 WQOG 114
DB 138 WKGK 141

RESULT 5
Q9UL72 PRELIMINARY; PRT; 118 AA.
AC
Q9UL72
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

SEQUENCE FROM N.A.
MEDLINE=98271739; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Werwe F.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035042; AAD56278.1; -.
DR PIR; S21205; S21205.
DR HSSP; P01783; IIGC.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 118
FT NON_TER 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 63.8%; Score 397.5; DB 2; Length 118;
Best Local Similarity 72.2%; Pred. No. 1e-32;
Matches 83; Conservative 9; Mismatches 18; Indels 5; Gaps 4;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 59
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTVSSNY-MNWSVRQAPGKLESV-SVTYSGSSY 58

QY 60 YNPSVKGRTITSRDKNFTYLNMSLRADTAFTVYCARGSHYFGHHFPAVWQOG 114
DB 59 YADSVKGRTITSRDKNFTYLNMSLRADTAFTVYCARDR--FGFPLFDYWGOG 111

RESULT 6
HV3E_HUMAN STANDARD; PRT; 120 AA.
ID HV3E_HUMAN
AC P01766;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG heavy chain V-III region BRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77117674; PubMed=65324; DOI=10.1016/0019-2791(76)90271-8;
RA Capra J.D., Hopper J.E.;
RT "Comparative studies on monotypic IGM lambda and IgG kappa from an
RT individual patient. III. The complete amino acid sequence of the VH
RT region of the IGM paraprotein.";
RL Immunohistochemistry 13:995-999 (1976).
CC -!- MISCELLANEOUS: This chain was obtained from IGM isolated from the
CC serum of a patient with malignant lymphoma of the Waldenström
CC type.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02049; M3HUEW.
DR HSSP; P01783; IIGC.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 111 Ig-like.
FT NON_TER 120
FT NON_TER 120
SQ SEQUENCE 120 AA; 13227 MW; D3F0428F7C2E6410 CRC64;

Query Match 63.6%; Score 396; DB 1; Length 120;
Best Local Similarity 65.0%; Pred. No. 1.5e-32;
Matches 80; Conservative 12; Mismatches 17; Indels 14; Gaps 3;
```

[illegible]

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RESULT 8
Q65ZC9
ID Q65ZC9 PRELIMINARY; PRT; 240 AA.
AC Q65ZC9;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
OS Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=C1q/7;
RC
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E.; Wing M.G.; Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL: Y13056; CAA73499.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF000047; Ig; 2.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00406; IGV; 2.
DR PROSITE: PS50835; IG_LIKE; 2.
FT NON TER 1
FT NON TER 240
FT NON TER 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 63.2%; Score 394; DB 2; Length 240;
Best Local Similarity 68.4%; Pred. No. 5e-32;
Matches 80; Conservative 11; Mismatches 16; Indels 10; Gaps 4

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| | | | | | |
|--------|------------------------------------------------------------|----------------------------------------|------------------------|--------------------------------------|-----|
| Qy | | 1 | EVLVSEGGGLVPGGSLRLSCA | VSGYSLITSGYSWNIROAPGKLEWVASIKYSGETK- | 59 |
| Dd | | 1 | QVLVSEGGGLVPGGSLRLSCA | SAGFTFS-YGMHWVRQAPGKLEWVAISYDGSNKY | 59 |
| Qy | | 60 | YNPSVKGRITISDDSKNTFYLO | WNLSRAEDTAVYYCARGSHYFGHHFAV--WGOG | 114 |
| Dd | | 60 | YADSVKGRFTISRDNKNLTLY | LQWNLSRAEDTAVYYCAR-----DWGDSLDPWGKG | 110 |
| RESULT | 9 | | | | |
| ID | Q6N089 | | | | |
| Q6N089 | | | PRELIMINARY; | PRT; 472 AA. | |
| AC | Q6N089; | | | | |
| DT | 05-JUL-2004 | (TEMBLrel. 27, Created) | | | |
| DT | 05-JUL-2004 | (TEMBLrel. 27, Last sequence update) | | | |
| DT | 05-JUL-2004 | (TEMBLrel. 27, Last annotation update) | | | |
| DE | Hypothetical protein DKFZp686P15220. | | | | |
| GN | Name=DKFZp686P15220; | | | | |
| OS | Homo sapiens (human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| OX | NCBI TaxID=9606; | | | | |


```
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA The German Human cDNA Consortium;
RG Wambutt R., Heubner D., Mewes H.W., Weil B., Anid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAB45781.1; -
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 63.2%; Score 394; DB 2; Length 472;
Best Local Similarity 66.7%; Pred. No. 1.1e-31;
Matches 78; Conservative 14; Mismatches 21; Indels 4; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTF-SDYAMHWVRQAPGKGLVWVSGISWNSGSA 78
Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTF-SDYAMHWVRQAPGKGLVWVSGISWNSGSA 78

Qy 60 YNPVSKGRITISRDTSKNTFYLMNSLRAETAVTYCAR--GSHYFGHWHFAVWGQ 114
Db 79 YADSVKGRFTISRDNKNSLYLQMNSLRAETALTYCAKEIQAHHFYFGYMDVWGQ 135

RESULT 10
HV3G_HUMAN STANDARD; PRT; 122 AA.
ID HV3G_HUMAN
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region CMM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain: location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -!- MISCELLANEOUS: This mu chain was isolated from the plasma of a patient with macroglobulinemia.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01772; 2FBA.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyroliidone carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyroliidone carboxylic acid.
FT NON_TER 122 122

SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 63.2%; Score 393.5; DB 1; Length 122;
Best Local Similarity 65.5%; Pred. No. 2.7e-32;
Matches 76; Conservative 15; Mismatches 22; Indels 3; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTF-SDYAMHWVRQAPGKGLVWVSGISWNSGSA 60
Db 1 QVELVESGGGVVZPGRSLRLSCAASGFTF-SDYAMHWVRQAPGKGLVWVSGISWNSGSA 59

Qy 61 NP-SVKGRITISRDTSKNTFYLMNSLRAETAVTYCAR--GSHYFGHWHFAVWGQ 114
Db 60 YADSVKGRFTISRDNKNSLYLQMNSLRAETAVTYCAR--GSHYFGHWHFAVWGQ 115

RESULT 11
Q9UL91 PRELIMINARY; PRT; 118 AA.
ID Q9UL91
AC Q9UL91;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -
DR PIR; PH0875; PH0875.
DR PIR; S21205; S21205.
DR PIR; S30531; S30531.
DR HSSP; P01783; 1IGC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
FT NON_TER 1 1
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 63.0%; Score 392.5; DB 2; Length 118;
Best Local Similarity 70.4%; Pred. No. 3.3e-32;
Matches 81; Conservative 10; Mismatches 19; Indels 5; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSS-YSNHWVRQAPGKGLVWVSGISWNSGSA 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSS-YSNHWVRQAPGKGLVWVSGISWNSGSA 59

Qy 60 YNPVSKGRITISRDTSKNTFYLMNSLRAETAVTYCAR--GSHYFGHWHFAVWGQ 114
Db 60 YADSVKGRFTISRDNKNSLYLQMNSLRAETAVTYCAR--GSHYFGHWHFAVWGQ 111

RESULT 12
Q6MZV7 PRELIMINARY; PRT; 473 AA.
ID Q6MZV7
AC Q6MZV7;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C11235.
GN Name=DKFZp686C11235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RG The German Human cDNA Consortium;
RA Bloecker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RM EMBL: BX640853; CAB45920.1; -
DR HSP; P01863; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 94762AB4C0BFC447 CRC64;

Query Match 62.8%; Score 391.5; DB 2; Length 473;
Best Local Similarity 64.4%; Pred. No. 1.9e-31;
Matches 76; Conservative 17; Mismatches 20; Indels 5; Gaps 3;

QY 1 EVLVRSGLGVQPGSLRLSCAVSGYSITSGYSNWIRQAPGKLEWVASIKYSGET-K 59
Db EIQVLVRSGLGVQPGSLRLSCAVSGFTFS-PENNVRQAPGKLEWLSVITRSGNTVY 78
QY 60 YNPSVKGRITISRDNSKNTFYLNNSLRADTAVYVCARGSHYFQHW---FAVWGQ 114
Db YADSLQGRFTISRDNARNSLYLNNSLRADTAVYVCARQNEHTSPWYPFDFYWGQ 136

RESULT 13

Q6GMV2 ID Q6GMV2 PRELIMINARY; PRT; 606 AA.
AC Q6GMV2
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RM EMBL: BC073758; AAH73758.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 606 AA; 66184 MW; B6B38B5114E4C55 CRC64;

Query Match 62.8%; Score 391.5; DB 2; Length 606;
Best Local Similarity 62.5%; Pred. No. 2.5e-31;
Matches 80; Conservative 13; Mismatches 20; Indels 15; Gaps 3;

QY 1 EVLVRSGLGVQPGSLRLSCAVSGYSITSGYSNWIRQAPGKLEWVASIKYSGE-TK 59
Db QVQLVRSGLGVQPGSLRLSCAVSGFTF-SDYMSWIRQAPGKLEWVSIVSSSYTN 78
QY 60 YNPSVKGRITISRDNSKNTFYLNNSLRADTAVYVCARGSH-----YFGHW 106
Db YADSVKGRFTISRDNAKNSLYLNNSLRADTAVYVCARGNGTAAAGRVVYAEYVVY 138
QY 107 HFAVWGQ 114
Db 139 GMDVWGQ 146

RESULT 14

Q96BB9 ID Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.":
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC015760; AAH15760.1; -;
 DR PIR: S05271; S05271.
 DR PIR: S24260; S24260.
 DR HSP; P01861; IADQ.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
 SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8E263D9 CRC64;

Query Match 62.8%; Score 391; DB 2; Length 597;
 Best Local Similarity 68.9%; Pred. No. 2.8e-31;
 Matches 82; Conservative 12; Mismatches 19; Indels 6; Gaps 4;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIKYS-GETK 59
 Db 20 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASISGSGGSTY 78
 Qy 60 YNPVSKGRITISRDTSKNTFYLNMSLRAEDTAVVYCA---RGSHYFGHW-HFAVWGQ 114
 Db 79 YADSVKGRFTISRDTSKNTFYLNMSLRAEDTAVVYCAKDPRGYSASGNTREDYWGQ 137

RESULT 15
 Q6MZQ6 PRELIMINARY; PRT; 475 AA.
 AC Q6MZQ6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686G11190.
 GN Name=DKFZp686G11190;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human esophagus tumor;
 RG The German Human cDNA Consortium;
 RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
 RA Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BX640947; CAB45972.1; -;
 DR HSP; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IGV; 2.
 DR SMART; SM00407; IGV; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 KW Hypothetical protein.
 SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 62.5%; Score 389.5; DB 2; Length 475;
 Best Local Similarity 65.0%; Pred. No. 3.1e-31;
 Matches 78; Conservative 13; Mismatches 22; Indels 7; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIKYS-ETK 59
 Db 20 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASISGSGVNTY 78
 Qy 60 YNPVSKGRITISRDTSKNTFYLNMSLRAEDTAVVYCARGSHYF-----GHWHFVWGQ 114
 Db 79 YADSVKGRFTISRDTSKNTFYLNMSLRAEDTAVVYCARADYRDYQVSPAYWYFDVWGEG 138

Search completed: June 3, 2005, 09:16:14
 Job time : 33.7497 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 08:53:28 ; Search time 7.09576 Seconds
(without alignments)
1545.812 Million cell updates/sec

Title: US-10-791-619-12

Perfect score: 625

Sequence: 1 EVQLVESGGGLVQPGSLRL.....YCARSHYFGHWHPAVWGQG 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 420.5 | 67.3 | 140 | 2 S70442 | Ig heavy chain pre |
| 2 | 420 | 67.2 | 140 | 2 S31588 | Ig heavy chain v r |
| 3 | 419 | 67.0 | 123 | 2 S31114 | Ig heavy chain - h |
| 4 | 417 | 66.7 | 138 | 2 S31666 | Ig heavy chain v r |
| 5 | 415.5 | 66.5 | 122 | 2 E36005 | Ig heavy chain v r |
| 6 | 415.5 | 66.5 | 128 | 2 S48797 | Ig heavy chain v r |
| 7 | 414 | 66.2 | 121 | 2 S31113 | Ig heavy chain - h |
| 8 | 410.5 | 65.7 | 122 | 2 S31117 | Ig heavy chain - h |
| 9 | 410.5 | 65.7 | 141 | 2 S31669 | Ig heavy chain - h |
| 10 | 410.5 | 65.7 | 147 | 2 I37780 | Ig variable region |
| 11 | 410 | 65.6 | 121 | 2 S31666 | Ig heavy chain v r |
| 12 | 410 | 65.6 | 121 | 2 G36005 | Ig heavy chain v r |
| 13 | 409 | 65.4 | 117 | 2 S36259 | Ig heavy chain v r |
| 14 | 409 | 65.4 | 125 | 2 S30531 | Ig heavy chain v r |
| 15 | 408 | 65.3 | 119 | 2 S31107 | Ig heavy chain - h |
| 16 | 407.5 | 65.2 | 137 | 2 S31701 | Ig heavy chain v r |
| 17 | 406 | 65.0 | 135 | 2 S31598 | Ig heavy chain v r |
| 18 | 405 | 64.8 | 140 | 2 S31686 | Ig heavy chain v r |
| 19 | 404 | 64.6 | 127 | 2 S31674 | Ig heavy chain - h |
| 20 | 403 | 64.5 | 132 | 2 S31603 | Ig heavy chain v r |
| 21 | 402 | 64.3 | 123 | 2 S26794 | Ig heavy chain v r |
| 22 | 402 | 64.3 | 130 | 2 S31601 | Ig heavy chain v r |
| 23 | 401.5 | 64.2 | 138 | 2 S31116 | Ig heavy chain - h |
| 24 | 401.5 | 64.2 | 139 | 2 S31674 | Ig heavy chain v r |
| 25 | 400.5 | 64.1 | 114 | 2 S46390 | Ig heavy chain v r |
| 26 | 400 | 64.0 | 119 | 2 S31108 | Ig heavy chain - h |
| 27 | 400 | 64.0 | 119 | 2 F36005 | Ig heavy chain v r |
| 28 | 400 | 64.0 | 134 | 2 S31679 | Ig heavy chain v r |
| 29 | 400 | 64.0 | 160 | 2 S05271 | Ig heavy chain pre |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 399.5 | 63.9 | 116 | 2 S31110 | Ig heavy chain - h |
| 31 | 399.5 | 63.9 | 124 | 2 S20782 | Ig heavy chain v r |
| 32 | 399 | 63.8 | 119 | 2 D36005 | Ig heavy chain v r |
| 33 | 399 | 63.8 | 130 | 2 P00098 | Ig heavy chain pre |
| 34 | 399 | 63.8 | 143 | 2 S23624 | Ig heavy chain v r |
| 35 | 398.5 | 63.8 | 114 | 2 S36280 | Ig heavy chain v r |
| 36 | 398.5 | 63.8 | 136 | 2 S31587 | Ig heavy chain v r |
| 37 | 397.5 | 63.6 | 122 | 2 PC2398 | anti-tetanus toxin |
| 38 | 397 | 63.5 | 117 | 2 S36270 | Ig heavy chain v r |
| 39 | 396.5 | 63.4 | 120 | 2 S48798 | Ig heavy chain v r |
| 40 | 396 | 63.4 | 119 | 2 C36005 | Ig heavy chain v r |
| 41 | 396 | 63.4 | 121 | 2 I55673 | Ig heavy chain - h |
| 42 | 396 | 63.4 | 121 | 2 S31104 | Ig heavy chain (su |
| 43 | 396 | 63.4 | 134 | 2 S31699 | Ig heavy chain v r |
| 44 | 395.5 | 63.3 | 114 | 2 S46391 | Ig heavy chain v r |
| 45 | 395 | 63.2 | 123 | 2 S38493 | Ig heavy chain - h |

ALIGNMENTS

RESULT 1

S70442

Ig heavy chain precursor V region (mu) - human (fragment)
C:Species: Homo sapiens (man)

C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C:Accession: S70442

R:Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelles, C.

Mol. Immunol. 29, 1363-1373, 1992

A>Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of fet

A:Reference number: S70442; MUID:93024508; PMID:1383695

A:Accession: S70442

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-140 <CUI>

A:Cross-references: UNIPROT:Q8WUK1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 420.5; DB 2; Length 140;
Best Local Similarity 73.0%; Pred. No. 6.1e-30;
Matches 84; Conservative 8; Mismatches 20; Indels 3; Gaps 3;

| | | |
|----|----|-------------------------------------------------------------|
| Qy | 1 | EVQLVESGGGLVQPGSLRLCAVSGYSITSGYSHNWIROAPGKLEWVASTYDGSTN- 59 |
| Db | 20 | QVQLVESGGGVQPGSLRLCAASGTFP-SNYGMHWVRQAPGKLEWVAFIRYDGSNKY 78 |
| Qy | 60 | YNPSVKGRITTSRDDSKNTFLQMSLRADTAVYVCARGSHYFGHWHPAVWGQG 114 |
| Db | 79 | YADSVKGRFTISRDNKNTLYLQMSLRADTAVYVCAR-DHIVGATFYDWGQG 132 |

RESULT 2

S31588

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31588

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.

submitted to the EMBL Data Library June 1992

A>Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31588

A:Accession: S31588

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-140 <CUI>

A:Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.2%; Score 420; DB 2; Length 140;
Best Local Similarity 71.3%; Pred. No. 6.7e-30;


```
Qy 60 YNPVKGRITISRDSDKNTFYLMNSLRADTAVTYCARGSHYF---CHWHF-----AVWG 112
Db 60 YADSVKGRFTISRDNKNTLYLMNSLRADTAVTYCARNYYDSSGYYYYGMDVWG 119

Qy 113 QG 114
Db 120 QG 121

RESULT 7
Ig heavy chain - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31113
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A>Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31113
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-121 <RAA>
A:Cross-references: EMBL:X62962
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.2%; Score 414; DB 2; Length 121;
Best Local Similarity 70.4%; Pred. No. 1.9e-29;
Matches 81; Conservative 14; Mismatches 18; Indels 2; Gaps 2;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIT-YDGSN 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS-YAMSVWRQAPGKLEWVASISGSGSTY 59

Qy 60 YNPVKGRITISRDSDKNTFYLMNSLRADTAVTYCARGSHYFCHWHFPAWVGQ 114
Db 60 YADSVKGRFTISRDNKNTLYLMNSLRADTAVTYCATDWFYGRSAFDIWGQ 114

RESULT 8
Ig heavy chain - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31117
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A>Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31117
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-122 <RAA>
A:Cross-references: EMBL:X62967
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 65.7%; Score 410.5; DB 2; Length 122;
Best Local Similarity 71.6%; Pred. No. 4e-29;
Matches 83; Conservative 9; Mismatches 21; Indels 3; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASITYDGSN- 59
Db 1 QVQLVESGGGLVQPGSLRLSCAASGFTFS-YGMEWVRQAPGKLEWVASIVTYDGSNKY 59

Qy 60 YNPVKGRITISRDSDKNTFYLMNSLRADTAVTYCARGSHYFCHWHF-HEAVWGQ 114
Db 60 YADSVKGRFTISRDNKNTLYLMNSLRADTAVTYCARDFFAPPNWSHFDIWGQ 115
```

RESULT 9

S31669
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31669
R:Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A>Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31669

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-141 <CDI>

A:Cross-references: EMBL:Z14212; NID:g30959; PIDN:CAA78581.1; PID:g30960

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 65.7%; Score 410.5; DB 2; Length 141;

Best Local Similarity 70.7%; Pred. No. 4.6e-29;

Matches 82; Conservative 13; Mismatches 18; Indels 3; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASITYDGS-TN 59

Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFS-YSMNVWRQAPGKLEWVSSISSSSYIY 78

Qy 60 YNPVKGRITISRDSDKNTFYLMNSLRADTAVTYCARGSHYFCHWHFPAWVGQ 114

Db 79 YADSVKGRFTISRDNKNTLYLMNSLRADTAVTYCARGHLTGKGYFDLWGRG 134

RESULT 10

I37780
Ig variable region (VDJ) (clone T20-11) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999

C:Accession: I37780; S25474

R:Demaision, C.; Chastagner, P.; Theze, J.; Zouali, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A>Title: Somatic diversification in the heavy chain variable region genes expressed by h

A:Reference number: A36876; MUID:94119917; PMID:8290556

A:Accession: I37780

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-147 <RES>

A:Cross-references: EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID:g33579

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:28-111/Domain: immunoglobulin homology <IMM>

Query Match 65.7%; Score 410.5; DB 2; Length 147;

Best Local Similarity 70.3%; Pred. No. 4.8e-29;

Matches 83; Conservative 12; Mismatches 18; Indels 5; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASITYDGSN- 59

Db 14 EVQLVESGGGLVQPGGSLRLSCAASGFTFS-YMWSVWRQAPGKLEWVANIKDQSEKY 72

Qy 60 YNPVKGRITISRDSDKNTFYLMNSLRADTAVTYCARGSHYFCHWHF---AVWGQ 114

Db 73 YADSVKGRFTISRDNKNTLYLMNSLRADTAVTYCARGEGWGLYYGYGMDVWGQ 130

RESULT 11

S19666

Ig heavy chain V region (VH3DJH4) - human

C:Species: Homo sapiens (man)

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C:Accession: S19666

R:Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,

J. Mol. Biol. 222, 581-597, 1991

| | | | | |
|-----------------------|------------------|--------------------|-----------|-------------|
| Query Match | 65.3%; | Score 408; | DB 2; | Length 119; |
| Best Local Similarity | 70.9%; | Pred. NO. 6.4e-29; | | |
| Matches 83; | Conservative 13; | Mismatches 13; | Indels 8; | Gaps 4 |

Qy 1 EVOLVESGGGLVOPGGSLRLSCAVSGYSITGYSWNWIRQAPGKLEWVASIT-YDGSTN 59
Db 1 EVOLVESGGGLVOPGGSLRLSCAVSGFTFSS-YAMSWVRQAPGKLEWVASISGGSTY 59
Qy 60 YNPSVKGRITISRDDSKNTFYLOMNSLRAEDTAVYYCAR--GSHYFGHHFAVMGQG 114
Db 60 YADSVKGRFTISRDNKNTLYLOMNSLRAEDTAVYYCAKDPGASY---FDYWGQG 112

Search completed: June 3, 2005, 09:17:51
Job time : 8.09576 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 08:31:37 ; Search time 32.7497 Seconds

(without alignments)
1782.523 Million cell updates/sec

Title: US-10-791-619-12

Perfect score: 625

Sequence: 1 EVQLVSGGGLVQPGGSLRL.....YCARSHYFGHHFAVWQG 114

Scoring table: BLOSUM62

Gapop 120.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | ID | Description |
|------------|-------|-------------|-------------------|---------------------|
| 1 | 412 | 65.9 | 2 Q6PJA4 | Q6pia4 homo sapien |
| 2 | 410 | 65.6 | 2 Q9UL90 | Q9ul90 homo sapien |
| 3 | 403.5 | 64.6 | 118 2 Q9UL72 | Q9ul72 homo sapien |
| 4 | 400.5 | 64.1 | 613 2 Q8WUK1 | Q8wuk1 homo sapien |
| 5 | 400 | 64.0 | 121 2 Q9UL71 | Q9ul71 homo sapien |
| 6 | 400 | 64.0 | 240 2 Q65ZC9 | Q65zc9 homo sapien |
| 7 | 400 | 64.0 | 466 2 Q6IN78 | Q6in78 homo sapien |
| 8 | 398.5 | 63.8 | 606 2 Q6GMY2 | Q6gmy2 homo sapien |
| 9 | 397 | 63.5 | 478 2 Q6PI81 | Q6pi81 homo sapien |
| 10 | 395 | 63.2 | 116 2 Q9UL93 | Q9ul93 homo sapien |
| 11 | 395 | 63.2 | 472 2 Q6N089 | Q6n089 homo sapien |
| 12 | 394.5 | 63.1 | 473 2 Q6MZV7 | Q6mzv7 homo sapien |
| 13 | 393.5 | 63.0 | 118 2 Q9UL91 | Q9ul91 homo sapien |
| 14 | 392.5 | 62.8 | 122 1 HV3JF HUMAN | P01768 homo sapien |
| 15 | 392.5 | 62.8 | 147 2 Q9Y509 | Q9y509 homo sapien |
| 16 | 392 | 62.7 | 493 2 Q6GMX2 | Q6gmxx2 homo sapien |
| 17 | 392 | 62.7 | 597 2 Q96BB9 | Q96bb9 homo sapien |
| 18 | 391 | 62.6 | 120 1 HV3JE HUMAN | P01766 homo sapien |
| 19 | 391 | 62.6 | 464 2 Q6MZU6 | Q6mzu6 homo sapien |
| 20 | 390 | 62.4 | 123 1 HV24 MOUSE | P01793 mus musculus |
| 21 | 387.5 | 62.0 | 116 1 HV05 CARAU | P19181 carassius a |
| 22 | 387.5 | 62.0 | 475 2 Q6MZQ6 | Q6mzq6 homo sapien |
| 23 | 387.5 | 62.0 | 573 2 Q8WU38 | Q8wu38 homo sapien |
| 24 | 384 | 61.4 | 493 2 Q8NCL6 | Q8ncl6 homo sapien |
| 25 | 384 | 61.4 | 499 2 Q8NSK4 | Q8nsk4 homo sapien |
| 26 | 383.5 | 61.4 | 112 2 Q9HCC1 | Q9hcc1 homo sapien |
| 27 | 383 | 61.3 | 117 1 HV3C HUMAN | P01764 homo sapien |
| 28 | 379 | 60.6 | 479 2 Q99M22 | Q99m22 mus musculus |
| 29 | 378.5 | 60.6 | 494 2 Q96K68 | Q96k68 homo sapien |
| 30 | 375 | 60.0 | 115 1 HV3F HUMAN | P01767 homo sapien |
| 31 | 375 | 60.0 | 121 1 HV3JF HUMAN | P01771 homo sapien |

| | | | | | |
|----|-------|------|-----|--------------|---------------------|
| 32 | 375 | 60.0 | 123 | 1 HV22 MOUSE | P01791 mus musculus |
| 33 | 374.5 | 59.9 | 119 | 1 HV37 MOUSE | P01807 mus musculus |
| 34 | 373.5 | 59.8 | 487 | 2 Q5ZVX0 | Q5zvx0 homo sapien |
| 35 | 372 | 59.5 | 119 | 1 HV31 HUMAN | P01770 homo sapien |
| 36 | 371.5 | 59.4 | 487 | 2 Q99KA4 | Q99ka4 mus musculus |
| 37 | 371 | 59.4 | 487 | 2 Q80Z17 | Q80zi7 mus musculus |
| 38 | 370 | 59.2 | 123 | 1 HV23 MOUSE | P01792 mus musculus |
| 39 | 370 | 59.2 | 137 | 1 HV46 MOUSE | P01822 mus musculus |
| 40 | 369.5 | 59.1 | 136 | 2 Q6LBQ5 | Q6lbq5 mus musculus |
| 41 | 368.5 | 59.0 | 544 | 2 Q6FJ95 | Q6fp95 homo sapien |
| 42 | 367.5 | 58.8 | 122 | 1 HV21 MOUSE | P01790 mus musculus |
| 43 | 367.5 | 58.8 | 465 | 2 Q6P6C4 | Q6p6c4 homo sapien |
| 44 | 367.5 | 58.8 | 479 | 2 Q6MZV6 | Q6mzv6 homo sapien |
| 45 | 367 | 58.7 | 119 | 2 Q920E7 | Q920e7 mus musculus |

ALIGNMENTS

RESULT 1

Q6PJA4 PRELIMINARY; PRT; 470 AA.

AC Q6PJA4;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C., Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
ET Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX Strausberg R.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC018747; AAH18747.1; -;
DR HSRF; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

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KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 65.9%; Score 412; DB 2; Length 470;
Best Local Similarity 72.4%; Pred. No. 9.5e-33;
Matches 84; Conservative 11; Mismatches 17; Indels 4; Gaps 4;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVGSYITSGYSWNIRQAPGKGLWEVASITYDGSNTY 60
Db 20 EVQLVESGGGLVQPGGSLRLSCVVGTFSS-YWMSWVRQAPGKGLWEVANIKDQSEKY 78

Qy 61 N-PSVKGRITISRDSDKNTFYLQNSLRADETAVYYCAR-GSHYFGHHFAVWGQ 114
Db 79 YVDSVKGRFTISRDNKSNLYLQNSLRADETAVYYCARDGSSWYRDW-FDPWGQ 133

RESULT 2
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035042; AAD56278.1; -.
DR PIR; S21205; S21205.
DR HSP; P01783; IIGC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 64.6%; Score 403.5; DB 2; Length 118;
Best Local Similarity 73.0%; Pred. No. 1.5e-32;
Matches 84; Conservative 9; Mismatches 17; Indels 5; Gaps 4;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVGSYITSGYSWNIRQAPGKGLWEVASITYD-GSTN 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTVSSNY-MNHWVRQAPGKGLSV-SVTYSGSSY 58

Qy 60 YNPSVKGRITISRDSDKNTFYLQNSLRADETAVYYCARGSHYFGHHFAVWGQ 114
Db 59 YADSVKGRFTISRDNKSNLYLQNSLRADETAVYYCARDR--PGEFLFDYWGQ 111

RESULT 4
Q8WUK1 PRELIMINARY; PRT; 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Heise F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Besak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalak U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RA Strausberg R.;
```

```
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 65.9%; Score 412; DB 2; Length 470;
Best Local Similarity 72.4%; Pred. No. 9.5e-33;
Matches 84; Conservative 11; Mismatches 17; Indels 4; Gaps 4;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVGSYITSGYSWNIRQAPGKGLWEVASITYDGSNTY 60
Db 20 EVQLVESGGGLVQPGGSLRLSCVVGTFSS-YWMSWVRQAPGKGLWEVANIKDQSEKY 78

Qy 61 N-PSVKGRITISRDSDKNTFYLQNSLRADETAVYYCAR-GSHYFGHHFAVWGQ 114
Db 79 YVDSVKGRFTISRDNKSNLYLQNSLRADETAVYYCARDGSSWYRDW-FDPWGQ 133

RESULT 2
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR PIR; S78486; S78486.
DR HSP; P01772; 2P84.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; E57FDD19086D07F CRC64;

Query Match 65.6%; Score 410; DB 2; Length 113;
Best Local Similarity 71.3%; Pred. No. 3.2e-33;
Matches 82; Conservative 9; Mismatches 14; Indels 10; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVGSYITSGYSWNIRQAPGKGLWEVASITYDGSNTN- 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTSS-YGMHWVRQAPGKGLWEVAFIRYDGSNKY 59

Qy 60 YNPSVKGRITISRDSDKNTFYLQNSLRADETAVYYCARGSHYFGHHFAVWGQ 114
Db 60 YADSVKGRFTISRDNKSNLYLQNSLRADETAVYYCAKDLNY-----WGQ 106

RESULT 3
Q9UL72 PRELIMINARY; PRT; 118 AA.
AC Q9UL72;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL: BC020240; AAH20240.1; --
DR PIR: F36005; F36005.
DR PIR: G36005; G36005.
DR PIR: PH1642; PH1642.
DR PIR: PH1643; PH1643.
DR PIR: PH1645; PH1645.
DR PIR: PH1646; PH1646.
DR PIR: PL0098; PL0098.
DR PIR: PL0120; PL0120.
DR PIR: S15590; S15590.
DR PIR: S31116; S31116.
DR PIR: S31119; S31119.
DR PIR: S70442; S70442.
DR HSP: P01861; 1ADQ.
DR PFAM: PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS0290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;

Query Match 64.1%; Score 400.5; DB 2; Length 613;
Best Local Similarity 67.5%; Pred. No. 1.8e-31;
Matches 81; Conservative 11; Mismatches 15; Indels 13; Gaps 4;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWIRQAPGKLEWVASITYDGSTN- 59
Db 20 QVQLVESGGGVQPGGSLRLSCAASGFTFSS-YGMHWVRQAPGKLEWVAVISYDGSNRY 78
QY 60 YNPYSVKGRITISRDSDKNTLYQMNSLRADTAVYTCARGSHYFGHWH-FAVWGQ 114
Db 79 YADSVKGRFTISRDNKNTLYQMNSLRADTAVYTCAR-----DWSEGVETFDINGQG 132

RESULT 5
Q9UL71 PRELIMINARY; PRT; 121 AA.
ID Q9UL71
AC Q9UL71
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035043; AAD56279.1; --
DR HSP: P01852; INFN.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER 1 121
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 64.0%; Score 400; DB 2; Length 121;
Best Local Similarity 68.7%; Pred. No. 3.4e-32;
Matches 79; Conservative 14; Mismatches 20; Indels 2; Gaps 2;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWIRQAPGKLEWVASITYD-GSTN 59
Db 1 EVQLVESGGGVQPGGSLRLSCAASGFTF-DGYAMHWVRQAPGKLEWVLSISGGGSTY 59

QY 60 YNPYSVKGRITISRDSDKNTLYQMNSLRADTAVYTCARGSHYFGHWHFAVWGQ 114
Db 60 YADSVKGRFTISRDNKNTLYQMNSLRADTAVYTCARGKVTIYDRFDINGQG 114

RESULT 6
Q65ZC9 PRELIMINARY; PRT; 240 AA.
ID Q65ZC9
AC Q65ZC9
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name-scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1q/7;
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies."
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL: Y13056; CAA73499.1; --
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR PFAM: PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON TER 1 240
FT NON TER 240 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 64.0%; Score 400; DB 2; Length 240;
Best Local Similarity 69.2%; Pred. No. 7.2e-32;
Matches 81; Conservative 12; Mismatches 14; Indels 10; Gaps 4;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWIRQAPGKLEWVASITYDGSTN- 59
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSS-YGMHWVRQAPGKLEWVAVISYDGSNRY 59
QY 60 YNPYSVKGRITISRDSDKNTLYQMNSLRADTAVYTCARGSHYFGHWHFAV--WQGG 114
Db 60 YADSVKGRFTISRDNKNTLYQMNSLRADTAVYTCAR-----DWGSDLPWCKG 110

RESULT 7
Q6IN78 PRELIMINARY; PRT; 466 AA.
ID Q6IN78
AC Q6IN78
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE IGHI1 protein.
GN Name=IGHI1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00407; IGL1; 3.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCDEB81076E CRC64;

Query Match 64.0%; Score 400; DB 2; Length 466;
Best Local Similarity 69.3%; Pred. No. 1.5e-31;
Matches 79; Conservative 12; Mismatches 19; Indels 4; Gaps 2;

QY 1 EVLVESGGGLVOPGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 EVLVESGGGLVOPGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 78

QY 61 NPSVKGRTITSDSKNTFYLMNSLRADTAVYTCARGSHYFGHMFVWGQ 114
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
79 ADSVKGRFTISRDNSKNTLYQMNSLRADTAVYTCARGNVV---PAAPWGQ 129

RESULT 8
Q6GMV2 O6GMV2 PRELIMINARY; PRT; 606 AA.
AC Q6GMV2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Schmutz J., Schmutz J., Schmutz J.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073758; AAH73758.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR Pfam; PF00047; IGL1; 4.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGL1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
KW Hypothetical protein.
SQ SEQUENCE 606 AA; 66184 MW; B6B38B5114E4C55 CRC64;

Query Match 63.8%; Score 398.5; DB 2; Length 606;
Best Local Similarity 63.3%; Pred. No. 2.8e-31;
Matches 81; Conservative 14; Mismatches 18; Indels 15; Gaps 3;

QY 1 EVLVESGGGLVOPGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASITVDGS-TN 59
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVLVESGGGLVOPGSLRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASITVDGS-TN 78

QY 60 YNPSVKGRTITSDSKNTFYLMNSLRADTAVYTCARGSHYFGHMFVWGQ 106
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
79 YADSVKGRFTISRDNSKNTLYQMNSLRADTAVYTCARGNVV---PAAPWGQ 138

QY 107 HFAVWGQ 114
Db |||||
139 GMDVWGQ 146

RESULT 9
Q6PI81 O6PI81 PRELIMINARY; PRT; 478 AA.
AC Q6PI81;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Patney J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish U., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG_C1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 63.5%; Score 397; DB 2; Length 478;
Best Local Similarity 65.3%; Pred. No. 3.1e-31;
Matches 81; Conservative 15; Mismatches 16; Indels 12; Gaps 4;

QY 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKLEWVASITYDGSNTY 60
Db 20 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKLEWVASIKDGSSEY 78

QY 61 N-PSYKGRITISRDSDSKNTFYLMNSLRAEDTAVYYCAR-----GSHYFGHWHFAV 110
Db 79 YVDSYKGRFTISRDNKNSLYLMNSLRAEDTAVYYCAREFESTMTTNADYY-YFYMDV 137

QY 111 WQQG 114
Db 138 WKGK 141

RESULT 10
Q9UL93
ID Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAE45781.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG_C1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 63.2%; Score 395; DB 2; Length 472;
Best Local Similarity 66.7%; Pred. No. 4.8e-31;
Matches 78; Conservative 16; Mismatches 19; Indels 4; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKLEWVASITYD-GSTN 59
Db 20 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKLEWVASISWNSGSA 78

QY 60 YNPSYKGRITISRDSDSKNTFYLMNSLRAEDTAVYYCAR--GSHYFGHWHFAVWQGG 114
Db 79 YADSYKGRFTISRDNKNSLYLMNSLRAEDTALYYCAKEIGHAHNFYYGYMDVWQGG 135

RESULT 12
Q6MZV7
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DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON TER 1
FT NON TER 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 63.2%; Score 395; DB 2; Length 116;
Best Local Similarity 70.2%; Pred. No. 1e-31;
Matches 80; Conservative 10; Mismatches 18; Indels 6; Gaps 3;

QY 2 VOLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKLEWVASITYDGSNTY 60
Db 1 VOLVESGGGVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKLEWVASISYDGSNKYY 59

QY 61 NPSYKGRITISRDSDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWQGG 114
Db 60 ADSYKGRFTISRDNKNSLYLMNSLRAEDTAVYYCAGG---GGGLGLGYWQGG 109
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RESULT 15
Q9Y509
ID Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Vh3 protein (Fragment).
GN Name=Vh3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1348-1353(1995).
DR EMBL; S80860; AAD14339.1; -.
DR HSSP; P01842; 1AOK.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER 147
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

Query Match 62.8%; Score 392.5; DB 2; Length 147;
Best Local Similarity 65.0%; Pred. No. 2.4e-31;
Matches 78; Conservative 15; Mismatches 20; Indels 7; Gaps 4;

Qy 1 EVQLVESGGGLVQPQGSRLRLSCAVSGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
Db 1 QVHLVESGGGVQPQKSLRLSCEASGFTF-STYGMVVRQAPGKGLDWVALISYDGSTQY 59

Qy 61 NP-SVKGRITISRDSDKNTLYLQMSLRAEDEVYVYCAKRGSHYF---GHWHFAV--WGQG 114
Db 60 YAGSVKGRFTISRDNSKNTLYLQMTSLRAVEDTAVYVYCAKDGNYFSDVGVYAGIDYWGQG 119

Search completed: June 3, 2005, 09:16:15
Job time : 33.7497 secs
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